

1
Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn. Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn.

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:44:40 ; Search time 538.767 Seconds
(without alignments)
756.808 Million cell updates/sec

Title: US-09-940-235-2_COPY_16_383

Perfect score: 1901

Sequence: 1 SQLVSVAGTVEGTNQDISL.....IITVMGKRPGENASYHLA 368

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 6730630 seqs, 1107998698 residues

Total number of hits satisfying chosen parameters: 6730630

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA Main:

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep.*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep.*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep.*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep.*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep.*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep.*
- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep.*
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- 35: /cgn2_6/ptodata/1/paa/US109_COMB.pep.*
- 36: /cgn2_6/ptodata/1/paa/US160_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	1901	100.0	413	29	US-10-360-101-264	Sequence 264, App
2	1901	100.0	413	29	US-10-360-101A-264	Sequence 264, App
3	1901	100.0	414	1	PCT-US93-09502-1	Sequence 1, Appli
4	1901	100.0	414	3	US-07-956-692A-9	Sequence 9, Appli
5	1901	100.0	414	5	US-08-128-299-1	Sequence 1, Appli
6	1901	100.0	414	18	US-09-471-349-2	Sequence 2, Appli
7	1901	100.0	414	24	US-09-940-235-2	Sequence 2, Appli
8	1901	100.0	414	32	US-10-631-558-2	Sequence 2, Appli
9	1901	100.0	440	22	US-09-791-537-45187	Sequence 45187, A
10	1875	98.6	401	20	US-09-658-681-1	Sequence 1, Appli
11	1875	98.6	413	20	US-09-658-681-2	Sequence 2, Appli
12	1875	98.6	414	18	US-09-438-136-252	Sequence 252, App
13	1875	98.6	414	20	US-09-633-516B-7	Sequence 7, Appli
14	1875	98.6	414	22	US-09-791-537-418	Sequence 418, App
15	1875	98.6	414	29	US-10-300-215-252	Sequence 252, App
16	1875	98.6	415	22	US-09-791-537-32688	Sequence 32688, A
17	1868.5	98.3	415	17	US-09-305-958-4	Sequence 4, Appli
18	1868.5	98.3	415	17	US-09-305-970-5	Sequence 5, Appli
19	1864	98.1	414	18	US-09-438-136-253	Sequence 253, App
20	1864	98.1	414	20	US-09-633-516B-8	Sequence 8, Appli
21	1864	98.1	414	29	US-10-300-215-253	Sequence 253, App
22	1859	97.8	440	22	US-09-791-537-45192	Sequence 45192, A
23	1845	97.1	413	9	US-08-567-943-12	Sequence 12, Appl
24	1845	97.1	413	24	US-09-919-703-12	Sequence 12, Appl
25	1822	95.8	362	22	US-09-791-537-43287	Sequence 23287, A
26	1819	95.7	384	20	US-09-658-681-4	Sequence 4, Appli
27	1815	95.5	372	20	US-09-658-681-3	Sequence 3, Appli
28	1741	91.6	440	30	US-10-415-182A-8298	Sequence 8298, Ap
29	1741	91.6	440	30	US-10-474-792-658	Sequence 658, App
30	1726	90.8	440	22	US-09-791-537-45189	Sequence 45189, A
31	1597	84.0	440	22	US-09-791-537-33832	Sequence 33832, A
32	1590	83.6	414	22	US-09-791-537-64009	Sequence 64009, A
33	1576	82.9	440	22	US-09-791-537-104248	Sequence 104248, A
34	708	37.2	138	22	US-09-791-537-12562	Sequence 12562, A
35	695	36.6	137	22	US-09-791-537-83460	Sequence 83460, A
36	620	32.6	128	22	US-09-791-537-83461	Sequence 83461, A
37	569	29.9	128	22	US-09-791-537-83463	Sequence 83463, A
38	557	29.3	128	22	US-09-791-537-83462	Sequence 83462, A
39	552	29.0	128	22	US-09-791-537-49654	Sequence 49654, A
40	429.5	22.6	400	22	US-09-791-537-83480	Sequence 83480, A
41	423	22.3	128	22	US-09-791-537-83467	Sequence 83467, A
42	419	22.0	128	22	US-09-791-537-83466	Sequence 83466, A
43	419	22.0	128	22	US-09-791-537-83466	Sequence 83466, A
44	417	21.9	128	22	US-09-791-537-83483	Sequence 83483, A
45	408	21.5	128	22	US-09-791-537-83483	Sequence 83483, A

ALIGNMENTS

RESULT 1
US-10-360-101-264
; Sequence 264, Application US/10360101
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10360,101
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 264
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of streptokinase

US-10-360-101-264

Query Match 100.0%; Score 1901; DB 29; Length 413;
Best Local Similarity 100.0%; Pred. No. 5e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 75

Qy 61 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKDGSVTLPTQPVQEF 135

Qy 121 LLSGHVRVRPYKEKPIQNOAKSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEKPIQNOAKSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 255

Qy 241 KKSGLNEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315

Qy 301 ASERNLDFRDLYPDPRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDHDTNRITIVYMGKRPEG 360
Db 316 ASERNLDFRDLYPDPRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDHDTNRITIVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 2

US-10-360-101A-264
; Sequence 264, Application US/10360101A
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Leenhouts, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673
; CURRENT APPLICATION NUMBER: US/10/360,101A
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: EP 02077060.8
; PRIOR FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 313
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 264
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence of streptokinase

US-10-360-101A-264

Query Match 100.0%; Score 1901; DB 29; Length 413;
Best Local Similarity 100.0%; Pred. No. 5e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 75

Qy 61 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKDGSVTLPTQPVQEF 135

Qy 121 LLSGHVRVRPYKEKPIQNOAKSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEKPIQNOAKSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 240
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Qy 241 KKSGLNEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315

Qy 301 ASERNLDFRDLYPDPRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDHDTNRITIVYMGKRPEG 360
Db 316 ASERNLDFRDLYPDPRDKAKLLYNNLDAGFIMDYTLTGKVEDNHDHDTNRITIVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 3

PCT-US93-09502-1
; Sequence 1, Application PC/TUS9309502
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the
; TITLE OF INVENTION: DNA Encoding Such Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09502
; FILING DATE: Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: 0609.3570001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2545
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both

PCT-US93-09502-1

Query Match 100.0%; Score 1901; DB 1; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFEDILTSRPAHGGKTEQGLSPKSPKFPATDSGAMSHKLE 75

Qy 61 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEOQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKDGSVTLPTQPVQEF 135

Qy 121 LLSGHVRVRPYKEKPIQNOAKSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEKPIQNOAKSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAIGDTIT 195

Qy 181 SQELLAQAQSILNKNHPCYTIYERDSSIVTHDNDIFRTILPMDQFTYRVKRNREQAYRIN 240

Db 196 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITLPMQDQFTYRVKREQAYRIN 255
QY 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
QY 301 ASERNLDFRDLYDPRDKAKLLYNNLDFAFGIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDPRDKAKLLYNNLDFAFGIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 375
QY 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 4

US-07-956-692A-9
; Sequence 9, Application US/07956692A
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; APPLICANT: Kussie, Paul
; APPLICANT: Farhami-Seren, Behnaz
; TITLE OF INVENTION: Recombinant Streptokinase Fragments with
; TITLE OF INVENTION: Decreased Antigenicity and Uses Thereof
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956.692A
; FILING DATE: 19921005
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Goldstein, Jorge A.
; REGISTRATION NUMBER: 29,021
; REFERENCE/DOCKET NUMBER: 0609.3570000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 833-7533
; TELEFAX: (202) 833-8716
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: both
; TOPOLOGY: both
; US-07-956-692A-9

Query Match 100.0%; Score 1901; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOLVSVAGTVEGTNODISLKFEEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNODISLKFEEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75
QY 61 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQPVQEF 135
QY 121 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDFFRPLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDFFRPLKDTKLLKTLAIGDTIT 195

QY 181 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITLPMQDQFTYRVKREQAYRIN 240
Db 196 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITLPMQDQFTYRVKREQAYRIN 255
QY 241 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
QY 301 ASERNLDFRDLYDPRDKAKLLYNNLDFAFGIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDPRDKAKLLYNNLDFAFGIMDYTLTGKVEDNHDNTRIIITVYMGKRPEG 375
QY 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 5

US-08-128-299-1
; Sequence 1, Application US/08128299
; GENERAL INFORMATION:
; APPLICANT: Reed, Guy L.
; TITLE OF INVENTION: Peptides Specifically Binding to Plasminogen And the
; TITLE OF INVENTION: DNA Encoding Such Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein and Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/128,299
; FILING DATE: Herewith
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sanzo, Michael A.
; REGISTRATION NUMBER: 36,912
; REFERENCE/DOCKET NUMBER: 0609.3570001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2545
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; STRANDEDNESS: both
; TOPOLOGY: both
; US-08-128-299-1

Query Match 100.0%; Score 1901; DB 5; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SOLVSVAGTVEGTNODISLKFEEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNODISLKFEEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75
QY 61 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEQLIANVHNSDDYFEVIDFASDATITDRNGKVFADKOGSVTLPTQPVQEF 135
QY 121 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDFFRPLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPYKEPIQNOAKSVDEYTVQFTPLNPDFFRPLKDTKLLKTLAIGDTIT 195
QY 181 SOELLAQAQSILNKNHPGTYIYERDSSIVTHNDIFRITLPMQDQFTYRVKREQAYRIN 240

Db 196 SQELLAQAQSILNKNHPGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 255
Qy 241 KKSGLNEEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLYDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 6
US-09-471-349-2
; Sequence 2, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sabni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-471-349-2

Query Match 100.0%; Score 1901; DB 18; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDISLKFFIDLTSRPAHGKTEQGLSPKSPKPPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFIDLTSRPAHGKTEQGLSPKSPKPPATDSGAMSHKLE 75
Qy 61 KADLLKAIQEOQLIANVHSNDYFEVIDFASDATITDRNGKYVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHSNDYFEVIDFASDATITDRNGKYVFADKDGSVTLPTQVQEF 135
Qy 121 LLSGHVRVRPKPKPIQNAQSVDEYTVQFTPLNPDDEFGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPKPKPIQNAQSVDEYTVQFTPLNPDDEFGLKDTKLLKTLAIGDTIT 195
Qy 181 SQELLAQAQSILNKNHPGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 240
Db 196 SQELLAQAQSILNKNHPGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 255
Qy 241 KKSGLNEEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLYDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

Db 376 ENASYHLA 383
RESULT 7
US-09-940-235-2
; Sequence 2, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT FILING DATE: 2002-04-09
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-940-235-2

Query Match 100.0%; Score 1901; DB 24; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDISLKFFIDLTSRPAHGKTEQGLSPKSPKPPATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFIDLTSRPAHGKTEQGLSPKSPKPPATDSGAMSHKLE 75
Qy 61 KADLLKAIQEOQLIANVHSNDYFEVIDFASDATITDRNGKYVFADKDGSVTLPTQVQEF 120
Db 76 KADLLKAIQEOQLIANVHSNDYFEVIDFASDATITDRNGKYVFADKDGSVTLPTQVQEF 135
Qy 121 LLSGHVRVRPKPKPIQNAQSVDEYTVQFTPLNPDDEFGLKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVRVRPKPKPIQNAQSVDEYTVQFTPLNPDDEFGLKDTKLLKTLAIGDTIT 195
Qy 181 SQELLAQAQSILNKNHPGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 240
Db 196 SQELLAQAQSILNKNHPGTYIYERDSSIVTHDNDIFRILPMDQEFYVRVKNRQAYRN 255
Qy 241 KKSGLNEEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVLKGEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRDLYDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLYDPRDKAKLLYNLDAGFINDYTLTGKVEDNHDNTNRIITVYMGKRPEG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383
RESULT 8
US-10-631-558-2
; Sequence 2, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait

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; APPLICANT: Rajagopal, Kammaral
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-10-631-558-2

Query Match      100.0%; Score 1901; DB 32; Length 414;
Best Local Similarity 100.0%; Pred. No. 5.1e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 75

Qy 61 KADLLKAIQEQLIANVHNSNDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQEQLIANVHNSNDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 135

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Db 136 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 195

Qy 181 SOELLAQAQSILNKNHGYTIYERDSSIVTHNDIFRTILPMDQEFYRVKNREQAYRIN 240
Db 196 SOELLAQAQSILNKNHGYTIYERDSSIVTHNDIFRTILPMDQEFYRVKNREQAYRIN 255

Qy 241 KKSGLNEEINNTDLISEKYVVLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVVLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315

Qy 301 ASERNLDFRDLVPRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDDTNRIITVYMGKRPEG 360
Db 316 ASERNLDFRDLVPRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDDTNRIITVYMGKRPEG 375

Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383

RESULT 9
US-09-791-537-45187
; Sequence 45187, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45187
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; LENGTH: 440
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-791-537-45187

Query Match      100.0%; Score 1901; DB 22; Length 440;
Best Local Similarity 100.0%; Pred. No. 5.6e-170;
Matches 368; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 42 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 101

Qy 61 KADLLKAIQEQLIANVHNSNDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 102 KADLLKAIQEQLIANVHNSNDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 161

Qy 121 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 180
Db 162 LLSGHVRVRPYKEKPIQNAQSVVEYTVQFTPLNPDDEFPRGLKDTLLKTLAIGDTIT 221

Qy 181 SOELLAQAQSILNKNHGYTIYERDSSIVTHNDIFRTILPMDQEFYRVKNREQAYRIN 240
Db 222 SOELLAQAQSILNKNHGYTIYERDSSIVTHNDIFRTILPMDQEFYRVKNREQAYRIN 281

Qy 241 KKSGLNEEINNTDLISEKYVVLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 282 KKSGLNEEINNTDLISEKYVVLKKEKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 341

Qy 301 ASERNLDFRDLVPRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDDTNRIITVYMGKRPEG 360
Db 342 ASERNLDFRDLVPRDKAKLLYNLDLAFGIMDYTLTGKVEDNHDDTNRIITVYMGKRPEG 401

Qy 361 ENASYHLA 368
Db 402 ENASYHLA 409

RESULT 10
US-09-658-681-1
; Sequence 1, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seraleña
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5
; CURRENT APPLICATION NUMBER: US/09/658,681
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
; US-09-658-681-1

Query Match      98.6%; Score 1875; DB 20; Length 401;
Best Local Similarity 98.6%; Pred. No. 1.4e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 60
Db 3 SOLVSVAGTVEGTNQDISLKFEIDLTSRPAHGGKTEQGLSPKSPKPFATDSGAMSHKLE 62

Qy 61 KADLLKAIQEQLIANVHNSNDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 63 KADLLKAIQEQLIANVHNSNDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 122
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Qy 121 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAGDIT 180
Db 123 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAGDIT 182
Qy 181 SQELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDOEFTYVRVKNRQAYRN 240
Db 183 SQELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDOEFTYVRVKNRQAYRN 242
Qy 241 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKVYDVDTNELLKSEQLLT 300
Db 243 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKVYDVDTNELLKSEQLLT 302
Qy 301 ASERNLDFRDIYDRDRKAKLLYNLDAFGIMDYTLTGKVEDNHDHDTNRITVYMGKRPEG 360
Db 303 ASERNLDFRDIYDRDRKAKLLYNLDAFGIMDYTLTGKVEDNHDHDTNRITVYMGKRPEG 362
Qy 361 ENASYHLA 368
Db 363 ENASYHLA 370
RESULT 11
US-09-658-681-2
; Sequence 2, Application US/09658681
; GENERAL INFORMATION:
; APPLICANT: Madrazo, Isis Del Carmen Torrens
; APPLICANT: Garcia, Jose De Jesus De La Fuente
; APPLICANT: Ojalvo, Ariana Garcia
; APPLICANT: Menendez, Alina Seraleña
; APPLICANT: Escalona, Elder Pupo
; APPLICANT: Masso, Julio Raul Fernandez
; APPLICANT: Griego, Martha De Jesus Gonzalez
; TITLE OF INVENTION: STREPTOKINASE MUTANTS
; FILE REFERENCE: Sequence Listings 1-14 re: 976-5
; CURRENT APPLICATION NUMBER: US/09/658,681
; CURRENT FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 413
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-09-658-681-2
Query Match 98.6%; Score 1875; DB 20; Length 413;
Best Local Similarity 98.6%; Pred. No. 1.4e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEOGLSPKSPKPFATDSGAMSHKLE 60
Db 3 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEOGLSPKSPKPFATDSGAMPHKLE 62
Qy 61 KADLLKAIQEQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKGSVTLPTQVQEF 120
Db 63 KADLLKAIQEQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKGSVTLPTQVQEF 122
Qy 121 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAGDIT 180
Db 123 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAGDIT 182
Qy 181 SQELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDOEFTYVRVKNRQAYRN 240
Db 183 SQELLAQAQSLNKNHPCYTIYERDSSIVTHDNDIFRILPMDOEFTYVRVKNRQAYRN 242
Qy 241 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKVYDVDTNELLKSEQLLT 300
Db 243 KKSGLNEEINNLTDLISEKYVYLKGEKPYDPFDRSHLKLFTIKVYDVDTNELLKSEQLLT 302
Qy 301 ASERNLDFRDIYDRDRKAKLLYNLDAFGIMDYTLTGKVEDNHDHDTNRITVYMGKRPEG 360
Db 303 ASERNLDFRDIYDRDRKAKLLYNLDAFGIMDYTLTGKVEDNHDHDTNRITVYMGKRPEG 362
Qy 361 ENASYHLA 368

Db 363 ENASYHLA 370
RESULT 12
US-09-438-136-252
; Sequence 252, Application US/09438136
; GENERAL INFORMATION:
; APPLICANT: CARR, Francis Joseph
; APPLICANT: ADAIR, Fiona Suzanne
; APPLICANT: HAMILTON, Anita Anne
; APPLICANT: CARTER, Graham
; TITLE OF INVENTION: METHOD FOR THE PRODUCTION OF
; NON-IMMUNOGENIC PROTEINS
; NUMBER OF SEQUENCES: 254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hale and Dorr L.L.P.
; STREET: 60 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: United States
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/438,136
; FILING DATE: 10-Nov-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/GB98/01473
; FILING DATE: 21-MAY-1998
; APPLICATION NUMBER: GB 9710480.6
; FILING DATE: 21-MAY-1997
; APPLICATION NUMBER: GB 9716197.0
; FILING DATE: 31-JUL-1997
; APPLICATION NUMBER: GB 9725270.4
; FILING DATE: 28-NOV-1997
; APPLICATION NUMBER: GB 9807751.4
; FILING DATE: 14-APR-1998
; APPLICATION NUMBER: US 60/067,235
; FILING DATE: 02-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Baker, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102286.395CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 526-6000
; INFORMATION FOR SEQ ID NO: 252:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
US-09-438-136-252
Query Match 98.6%; Score 1875; DB 18; Length 414;
Best Local Similarity 98.6%; Pred. No. 1.5e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEOGLSPKSPKPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDLSLKFFELDLTSRPAHGKTEOGLSPKSPKPFATDSGAMPHKLE 75
Qy 61 KADLLKAIQEQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKGSVTLPTQVQEF 120
Db 76 KADLLKAIQEQLIANVHNSDDYFEVIDPASDATITDRNGKVYFADKGSVTLPTQVQEF 135
Qy 121 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAGDIT 180
Db 136 LLSGHRVRPYKEPIQNAQSVDEYTVQFTPLNPDHDDFRPGLKDTKLLKTLAGDIT 195


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; PRIOR APPLICATION NUMBER: WO PCT/GB98/01473
; PRIOR FILING DATE: 1998-05-21
; PRIOR APPLICATION NUMBER: GB 9710480.6
; PRIOR FILING DATE: 1997-05-21
; PRIOR APPLICATION NUMBER: GB 9716197.0
; PRIOR FILING DATE: 1997-07-31
; PRIOR APPLICATION NUMBER: GB 9725270.4
; PRIOR FILING DATE: 1997-11-28
; PRIOR APPLICATION NUMBER: GB 9807751.4
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: US 60/067,235
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 254
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 252
; LENGTH: 414
; TYPE: PRT
; ORGANISM: Streptococcus equisimilis
US-10-300-215-252

Query Match          98.6%; Score 1875; DB 29; Length 414;
Best Local Similarity 98.6%; Pred. No. 1.5e-167;
Matches 363; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SOLVSVAGTVEGTNQDISLKFFIEDLTSRPAHGGKTEQGLSPKSPFATDSGAMSHKLE 60
Db 16 SOLVSVAGTVEGTNQDISLKFFIEDLTSRPAHGGKTEQGLSPKSPFATDSGAMPHKLE 75
Qy 61 KADLLKAIQQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 120
Db 76 KADLLKAIQQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEF 135
Qy 121 LLSGHVVRPYKKEPIQNAQKSVDEVYTVQFTPLNPDDDDPRPGKDTKLLKTLAIGDTIT 180
Db 136 LLSGHVVRPYKKEPIQNAQKSVDEVYTVQFTPLNPDDDDPRPGKDTKLLKTLAIGDTIT 195
Qy 181 SQELLAQAQSILNKNHFGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYRIN 240
Db 196 SQELLAQAQSILNKNHFGYTIYERDSSIVTHDNDIFRTILPMDQEFYRVKNREQAYEIN 255
Qy 241 KKSGLNEEINNTDLISEKYVYLKKGKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 300
Db 256 KKSGLNEEINNTDLISEKYVYLKKGKPYDPFDRSHLKLFTIKYVDVDTNELLKSEQLLT 315
Qy 301 ASERNLDFRLYDRDKAKLLYNLDAGFIMDYTLTGKVEDNHDHTNRIITVYMGKRPBG 360
Db 316 ASERNLDFRLYDRDKAKLLYNLDAGFIMDYTLTGKVEDNHDHTNRIITVYMGKRPBG 375
Qy 361 ENASYHLA 368
Db 376 ENASYHLA 383
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Job time : 540.767 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:21:37 ; Search time 6024.11 Seconds
(without alignments)
2477.164 Million cell updates/sec

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Perfect score: 1901

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1901	100.0	1245	40	US-09-940-235-1	Sequence 1, Appl
3	1901	100.0	1245	57	US-10-631-558-1	Sequence 1, Appl
4	1901	100.0	1254	25	US-09-569-920-2	Sequence 2, Appl
5	1901	100.0	1327	21	US-09-471-349-6	Sequence 6, Appl
6	1901	100.0	1327	40	US-09-940-235-6	Sequence 6, Appl
7	1901	100.0	1327	57	US-10-631-558-6	Sequence 6, Appl
8	1901	100.0	1377	21	US-09-471-349-5	Sequence 5, Appl
9	1901	100.0	1377	40	US-09-940-235-5	Sequence 5, Appl
10	1901	100.0	1377	57	US-10-631-558-5	Sequence 5, Appl
11	1901	100.0	1541	21	US-09-471-349-9	Sequence 9, Appl
12	1901	100.0	1541	40	US-09-940-235-9	Sequence 9, Appl
13	1901	100.0	1541	57	US-10-631-558-9	Sequence 9, Appl
14	1901	100.0	1661	21	US-09-471-349-10	Sequence 10, Appl
15	1901	100.0	1661	40	US-09-940-235-10	Sequence 10, Appl
16	1901	100.0	1661	57	US-10-631-558-10	Sequence 10, Appl
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18	1901	100.0	1782	40	US-09-940-235-11	Sequence 11, Appl
19	1901	100.0	1782	57	US-10-631-558-11	Sequence 11, Appl
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21	1901	100.0	2096	40	US-09-940-235-12	Sequence 12, Appl
22	1901	100.0	2096	57	US-10-631-558-12	Sequence 12, Appl
23	1901	100.0	8893	25	US-09-658-920-3	Sequence 3, Appl
24	1875	98.6	1209	28	US-09-658-920-11	Sequence 11, Appl
25	1875	98.6	1245	6	US-08-145-684-1	Sequence 1, Appl
26	1875	98.6	1245	28	US-09-658-681-12	Sequence 12, Appl
27	1875	98.6	1245	37	US-09-882-509-3	Sequence 3, Appl
28	1819	95.7	1158	28	US-09-658-681-14	Sequence 14, Appl
29	1815	95.5	1122	28	US-09-658-681-13	Sequence 13, Appl
30	1741	91.6	1320	53	US-10-415-182A-8297	Sequence 8297, Ap
31	1741	91.6	1323	54	US-10-474-792-657	Sequence 657, App
32	140.5	7.4	7155	12	US-08-761-184-674	Sequence 674, App
33	140.5	7.4	7155	13	US-08-821-931-674	Sequence 674, App
34	140.5	7.4	7155	14	US-08-993-002A-3325	Sequence 3325, Ap
35	140.5	7.4	7155	51	US-10-335-977-3325	Sequence 3325, App
36	138.5	7.3	7320	12	US-08-761-184-503	Sequence 503, App
37	138.5	7.3	7320	13	US-08-821-931-503	Sequence 503, App
38	138.5	7.3	7320	14	US-08-993-002A-3326	Sequence 3326, Ap

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Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 406 TTGCTAAGCGGACATGTCGGGTAGACCATATAAGAAACCAACCATACAAACCAAGCG 465
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 466 AAATCTGTGTGATGGAATATCTGACAGTTTACTCCCTTAAACCCCTGATGACGATTTT 525
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
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Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 586 TCTCAAGAAATCTAGCTCAAGCAAAAGCAATTTTAAACAAACCAACCCAGGCTATACG 645
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 646 ATTTATGACGTGACTCTCTCAATCGTCACTCATGACATGACATTTTCCGTCAGCATTTTA 705
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 706 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAAACCAAGCTTATAGATCAAT 765
Qy 241 LysLysSerGlyLeuAsnGluGluLeuAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 766 AAAAAATCTGCTCGAATGAAGAATAAACCACTGACCTGATCTCTGAGAAATATTATAC 825
Qy 261 ValLeuLysLysGlyLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 826 GTCCTTAAAAAGGGGAAACCGGTATGATCCCTTTGATCGCAGTCACTTCGAACTGTTC 885
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 886 ACCATCAATACGTTGATGTCATACCAACCAAGAAATGCTTAAAGGTGACGAGCTCTTACA 945
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 946 GCTACGCAACGTAATCTAGACTTCAGAGATTTATACGATCTCTGCTGATAAGGCTAAACTA 1005
Qy 321 LeuTyrAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1006 CTCACAAACATCTCGATGCTTTTGGTATTATGACTATACCTTAACCTGGAAGATGAG 1065
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1066 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATATGGCAAGCGACCGAAGGA 1125
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1126 GAGAATGCTAGCTATCATTTAGCC 1149

RESULT 2

US-09-940-235-1

; Sequence 1, Application US/09940235

; GENERAL INFORMATION:

; APPLICANT: Kumar, Rajesh

; APPLICANT: Sabni, Girish

; APPLICANT: Roy, Chait

; APPLICANT: Rajagopal, Kammar

; APPLICANT: Nihalani, Deepak

; APPLICANT: Sundaram, Vasudha

; APPLICANT: Yadav, Mahavir

; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

; TITLE OF INVENTION: PROTEIN

; FILE REFERENCE: 07064-009002

; CURRENT APPLICATION NUMBER: US/09/940,235

; CURRENT FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 09/471,349

; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1242)
US-09-940-235-1

Alignment Scores:

Pred. No.:	5,79e-186	Length:	1245
Score:	1901.00	Matches:	368
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	40	Gaps:	0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-1 (1-1245)

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Db 46 AGCCAAATAGTTGTTAGCGTTGCTGCTACTGTTGAGGGGACGAATCAAGACATTAAGTCTT 105
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 106 AAATTTTGAATCGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 165
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyValAlaMetSerHisLysLeuGlu 60
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Qy 61 LysAlaAspLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
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Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 286 GACTACTTTGAGGTCAATGATTTTGCAGAGCGATGCAACCATCTACTGATCGAAACGCAAG 345
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 346 GCTACTTTGCTGCAAAAGATGGTTTCGGTAACCTTTCGCCGACCAACCTGTCCAAAGATTT 405
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 406 TTGCTAAGCGGACATGTCGGGTTAGACCATATAAGAAACCAACCAATACAAACCAAGCG 465
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
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Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
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Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 586 TCTCAAGAAATCTAGCTCAAGCAAAAGCAATTTTAAACCAAAACCAACCCAGGCTATACG 645
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 646 ATTTATGACGTGACTCTCTCAATCGTCACTCATGACATGACATTTTCCGTCAGCATTTTA 705
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 706 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAAACCAAGCTTATAGATCAAT 765
Qy 241 LysLysSerGlyLeuAsnGluGluLeuAsnThrAspLeuIleSerGluLysTyrTyr 260

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Db 766 AAAAAATCTGGTCTGAATGAAGAAATAAACCAACACTGACCTGATCTCTGAGAAATATTAC 825
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Db 826 GTCTTAAAAAAGGGGAAAGCCGATGATCCCTTTGATCCAGTCACCTTGAACCTGTTTC 885
Qy 281 ThrileLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 886 ACCATCAATACGTTGATGTCGATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACA 945
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 946 GCTAGCGAACCTAACTTAGACTTCAGAGATTATATACGATCTCTGATGAAGGCTAAACCTA 1005
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyLeuMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1006 CTCTACAAACATCTCGATGCTTTGGTATTATGACTATATACCTTAACCTGGGAAAAAGTAGAG 1065
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RESULT 3

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US-10-631-558-1
; Sequence 1, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN/3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1245
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1242)
US-10-631-558-1
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Alignment Scores:
Pred. No.: 5,79e-186 Length: 1245
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0
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US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-1 (1-1245)
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Db 46 AGCCAAATAGTGTGTAGCGTTGCTGGTACTGTGTAGGGGACGAATCAAGACATTAGTCTT 105
Qy 21 LysPheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 106 AATTTTTTGAATTCGATCTAACATCACGACTGCTCATGAGGAGAAAGACAGACGACG 165
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 166 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGTCACATAAATTGAG 225
Qy 61 LysAlaAspLeuLysAlaIleGlnGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 226 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTTGATCGCTAACGTCACACAGTAA 285
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 286 GACTACTTTGAGGTCATTTGCAAGCGATGCAACATTTACTGATCGAAACCGCAAG 345
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 346 GTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGCCGACCCCAACCTGTCCAAGATT 405
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 406 TTGCTAAGCGGACATGTGCGCGTTAGACCATATAAGAAACCAATACAAACCAAGCG 465
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 466 AAATCTGTTGATGGGAATATACTGTACAGTTTACTCCCTTAACCCCTGATGACCATTC 525
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 526 AGACCAAGTCTCAAGATACCTAAGCTATTGAAACACATAGCTATCGGTGACACCATCA 585
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 586 TCTCAAGAATTACTAGCTCAAGCACAAGCATTTTAAACAAAAACCAACCCAGCTATACG 645
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 646 ATTTATGAACGTGACTCTCTCAATCGTCACTCATGACATGACATTTTCGTACGATTTTA 705
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 706 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAAACAAGCTTATAGGATCAAT 765
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 766 AAAAAATCTGGTCTGAATGAAGAAATAAACCAACACTGACCTGATCTCTGAGAAATATTAC 825
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
Db 826 GTCCTTAAAAAAGGGGAAAGCCGATGATCCCTTTGATCGCGATCCTTTGAAACTGTTC 885
Qy 281 ThrileLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 886 ACCATCAATACGTTGATGTCGATACCAACGAATTGCTTAAAAAGTGAGCAGCTCTTAACA 945
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 946 GCTAGCGAACCTAACTTAGACTTCAGAGATTATATACGATCTCTGATGAAGGCTAAACCTA 1005
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyLeuMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1006 CTCTACAAACATCTCGATGCTTTGGTATTATGACTATATACCTTAACCTGGGAAAAAGTAGAG 1065
Qy 341 AspAsnHisAspAspThrAsnArgileThrValTyrMetGlyLysArgProGluGly 360
Db 1066 GATPAATCAGATGACACCAACCGTATCATACCGTTTATATGGCGAAGCGACCCGAGGA 1125
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
```

Db 1126 GAGATGCTAGCTATCATTTAGCC 1149

RESULT 4
US-09-569-920-2
; Sequence 2, Application US/09569920
; GENERAL INFORMATION:
; APPLICANT: Reddy, Vemuri B.
; TITLE OF INVENTION: VASODILATOR-THROMBOLYTIC FUSION PROTEIN
; TITLE OF INVENTION: AND CONJUGATES
; FILE REFERENCE: 10284-026001
; CURRENT APPLICATION NUMBER: US/09/569,920
; PRIOR FILING DATE: 2000-05-11
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-09-569-920-2

Alignment Scores:
Pred. No.: 5.85e-186 Length: 1254
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-569-920-2 (1-1254)

Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspSerLeu 20
Db 52 AGCCAAATAGTTGTTAGGTTGCTGCTACTGTTGAGGGGAGCAATCAAGACATTAGTCTT 111

Qy 21 LysPheGluLeuAspLeuThrSerArgProLalaHisGlyGlyThrGluGlnGly 40
Db 112 AAAATTTTGAATCGATCTTAACATCAGCCTGCTCATGGAGGAAAGACAGAGCAAGGC 171

Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 172 TTAAGTCCAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTCTCAATAAACTTGG 231

Qy 61 LysAlaAspLeuLeuLysAlaGlnGluGlnLeuLeuAlaAsnValHisSerAsnAsp 80
Db 232 AAAGTGACTTACTAAAGGCTATTCAAGACAATGATCGCTAACGTCACAGTAACGAC 291

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 292 GACTACTTTGAGTTCATTTGTTTGAAGCGATGCAACCATTTACTGATCGAAACGGCAAG 351

Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 352 GTCTACTTTGCTGACAAAGATGTTGCGTAACCTTGGCGACCAACCTGTCCAAAGATT 411

Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 412 TTGCTAAGCGGACATGTCGCGGTAGACCATATAAAGAAACCAATCAAAACCAAGCG 471

Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 472 AAATCTGTTGATGGGAATATACGTACAGTTTACTCCCTTAACCCCTGATGACGATTC 531

Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 532 AGACGAGTCTCAAGATACTAAGCTATTGAAACACACTAGCTATCGGTGACACCATACA 591

Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 592 TCTCAAGAAATTTAGTCTCAAGCAAGCAAGCAATTTTAAACAAAAACCCAGGCTATACG 651

Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220

Db 652 ATTTATGACGTGACTCCTCAATCCTCACTCATGACAAATGACATTTTCGTCAGATTTTA 711

Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 712 CCAATGGATCAAGAGCTTTACTTACCGTGTAAATAATCGGAACAAGCTTATAGGATCAAT 771

Qy 241 LysLysSerGlyLeuAsnGluLeuIleAsnThrAspLeuLeuIleSerGluLysTyrTyr 260
Db 772 AAAAATCTGGTCTGAATCAAGAAATAAACACACACTGACCTGATCTCTGAGAAATATTAC 831

Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 832 GTCCCTTAAAAAAGGGGAAAGCCGATGATCCCTTTGATCGCAGTCACCTTGAACCTGTT 891

Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 892 ACCATCAATACGTTGATGTCGATACCAACGAATGCTTAAAGATGAGCAGCTCTTAAACA 951

Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 952 GCTAGCGAAGCTAACTTAGACTTCAGAGATTTTATACGATCCTCGTGATAAGGCTAACTA 1011

Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1012 CTCTACAAACAATCTCGATGCTTTTGGTATTATGAGCTATACCTTAACTGGAAGTAGAG 1071

Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1072 GATATACGATGACCAACCGTATCATACCGTTTATATGGCAAGCGACCCGAAGGA 1131

Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1132 GAGATGCTAGCTATCATTTAGCC 1155

RESULT 5
US-09-471-349-6
; Sequence 6, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-6

Alignment Scores:
Pred. No.: 6.28e-186 Length: 1327
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-471-349-6 (1-1327)

```
Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 128 AGCAATTTGGTTGTAGCGTTGCTGGTACTGTTGAGGGGACGATCAAGACATTAGTCTT 187
Qy 21 LysPhePheGluLeuAspLeuThrSerArgProAlaHisGlyGlyLeuThrGluGlnGly 40
Db 188 AAATTTTGAATTCGATCTAAACATCAGCCTCTCATGAGGAGAAACAGACAGCAAGGC 247
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 248 TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGGATGTCACATAAACTTGAG 307
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 308 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTGATCGTACGTCACAGTAAACGAC 367
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 368 GACTACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCATTAAGTATCGAAACGGCAAG 427
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 428 GTCTACTTTGCTGCAAAAGATGGTTCGGTAACCTTGGCGACCCCAACCTGTCCAGAATTT 487
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 488 TTGCTAAGCGGACATGTGCGGTTAGACCATTATAAGAAACCAACCAATCAAAACCAAGCG 547
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 548 AAATCTGCTGATGGGAATATCTGTCAGTTTACTCCCTTAAACCCCTGATGACGATTC 607
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 608 AGACCAAGTCTCAAGATATCTAAGCTATTGAAACACACTAGTATCGGTGACACCATCACA 667
Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 668 TCTCAAGAAATTACTAGTCTCAAGCAAAAGCAATTTTAAACAAACCCACCGGCTATACG 727
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 728 ATTTATGACGTGACTCTCAATCGTCACTCATGACAAATGACATTTTCCGTACGATTTTA 787
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 788 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAAATCGGAAACAAAGCTTATAGGATCAAT 847
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 848 AAAAATCTGCTCGAATGAAGAAATTAACAACTGACCTGATCTCTGAGAAATATTAC 907
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 908 GTCCTTAAAAAGGGGAAAGCCGTATGATCCCTTCATCGACGTCACTTGAACCTGTC 967
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 968 ACCATCAATACGTTGATGCGATACCAACGAATTGCTAAAAAGTGACGCTCTTAACA 1027
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1028 GCTAGCGAAAGTAACTTAGACTTCAGAGATTATACCATCTCTGATGATGAGGCTTAAACTA 1087
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1088 CTCTACAAACATCTCGATGCTTTTGGTATTATGACTATACCTTAACTGGAAGATAGAG 1147
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1148 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATATGGGCAAGCGACCGCAAGGA 1207
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
```

```
Db 1208 GAGAATGCTAGCTATCATTTAGCC 1231
RESULT 6
US-09-940-235-6
; Sequence 6, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sabni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1327
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-940-235-6
Alignment Scores:
Pred. No.: 6,28e-186 Length: 1327
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-6 (1-1327)
Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 128 AGCAATTTGGTTGTAGCGTTGCTGGTACTGTTGAGGGGACGATCAAGACATTAGTCTT 187
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLeuThrGluGlnGly 40
Db 188 AAATTTTGAATTCGATCTAAACATCAGCCTCTCATGAGGAGAAACAGACAGCAAGGC 247
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 248 TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGGATGTCATAAACTTGAG 307
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 308 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTGATCGTACGTCACAGTAAACGAC 367
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 368 GACTACTTTGAGGTCATTGATTTTGCAAGCGATGCAACCATTAAGTATCGAAACGGCAAG 427
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 428 GTCTACTTTGCTGCAAAAGATGGTTCGGTAACCTTGGCGACCCCAACCTGTCCAGAATTT 487
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 488 TTGCTAAGCGGACATGTGCGGTTAGACCATTATAAGAAACCAACCAATCAAAACCAAGCG 547
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
```

```
Db 548 AAATCTGTTGATGTGGAATATATCTGTACAGTTTACTCCCTTAAACCCGTGATGACGATTTTC 607
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 608 AGACCAGTCTCAAGATACTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA 667
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 668 TCTCAAGAAATTACTAGCTCAAGCACAAGCAATTTTAAACAAAACCCAGGCTATACG 727
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 728 ATTTATGAACGTGACTCTCAATCGTCTCATGCAATGACATTTTCCGTACGATTTTA 787
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 788 CCAATGGATCAAGAGTTTACTTACCGTGTATAAATCGGAACAAGCTTATAGGATCAAT 847
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrThr 260
Db 848 AAAAAATCTGCTCGAATGAAGAAATAAACCAACTGACCTGATCTCTGAGAAATATTAC 907
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 908 GTCTCTAAAAAAGGGGAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAACCTGTTTC 967
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 968 ACCATCAAAATACGTTGATGTCGATACCAACCAAGTGTCTAAAGTGAGCAGCTCTTAACA 1027
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1028 GCTAGGACGTAAGTACTAGACTTCAGAGATTATACGATCTCTCGTAAAGCTAAACTA 1087
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1088 CTCTACAAATCTCGATGCTTTGGTATTATGGACTATACCTTAACTGGGAAAGTAGAG 1147
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1148 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATGGGCAAGCGACCCGAAGGA 1207
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1208 GAGAACTGCTAGCTATCATTTAGCC 1231
```

RESULT 7

```
US-10-631-558-6
; Sequence 6, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
```

; LENGTH: 1327

; TYPE: DNA

; ORGANISM: Streptococcus equisimilis

US-10-631-558-6

Alignment Scores:

Pred. No.:	6,286-186	Length:	1327
Score:	1901.00	Matches:	368
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	57	Gaps:	0

US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-6 (1-1327)

```
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 128 AGCCAAATGGTGTGTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTT 187
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 188 AAATTTTGAATCGATCTACATCAGCCTGCTCATGGAGGAAAGACAGAGCAGGC 247
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyValaMetSerHisLysLeuGlu 60
Db 248 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGCGATGTCACATAAATTGAG 307
Qy 61 LysAlaAspLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 308 AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTTGATCGCTAAAGCTCCACAGTAACGAC 367
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 368 GACTACTTTGAGTCAATGATTTTGCACGCGATGCAACCAITACTGATCGAAACGCGAAG 427
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 428 GTCTACTTTGCTGACAAAGATGTTTCGGTAACCTTTGCCGACCAACCTCTCCAGAAATTT 487
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 488 TTGCTAAAGCGACATGTCGCGTTAGACCATATAAGAAACCAACCAATACAAACCAAGCG 547
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspAspPhe 160
Db 548 AAATCTGTTGATGTGGAATATATCTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTTC 607
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 608 AGACCAGTCTCAAGATACTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA 667
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 668 TCTCAAGAAATTACTAGCTCAAGCACAAGCAATTTTAAACAAAACCCAGGCTATACG 727
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 728 ATTTATGAACGTGACTCTCAATCGTCTCATGCAATGACATTTTCCGTACGATTTTA 787
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 788 CCAATGGATCAAGAGTTTACTTACCGTGTATAAATCGGAACAAGCTTATAGGATCAAT 847
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrThr 260
Db 848 AAAAAATCTGCTCGAATGAAGAAATAAACCAACTGACCTGATCTCTGAGAAATATTAC 907
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 908 GTCTCTAAAAAAGGGGAAAGCCGTATGATCCCTTTGATCGCAGTCACTTGAACCTGTTTC 967
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
```


Db 968 ACCATCAATACGTTGATGTGATACCAACGAATTGCTAAAGAGTGAGCAGCTCTTAACA 1027
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLeuAlaLysLeu 320
Db 1028 GCTAGCGAACGTAACCTTAGACTTCAGAGATTATACGATCTCGTGATAAGCGCTAAACTA 1087
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1088 CTCTACAAACATCTCGATCTTTTGGTATTATGACATATACCTTAACCTGGAAGAGTAGAG 1147
Qy 341 AspAsnHisAspAspThrAsnArgIleThrValTyrMetGlyLysArgProGluGly 360
Db 1148 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATATGGCGAAGCGACCGAAGGA 1207
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1208 GAGAATGCTAGCTATCATTTTAGCC 1231

RESULT 8

US-09-471-349-5
; Sequence 5, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahn, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-471-349-5

Alignment Scores:
Pred. No.: 6.57e-186 Length: 1377
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-471-349-5 (1-1377)

Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 178 AGCCAAATGGTGTGTAGCTTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTT 237
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyLysThrGluGlnGly 40
Db 238 AAATTTTGGATCGATCTACATCATCAGCCTGCTATGGAGGAGAAAGACAGACGAGGC 297
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 298 TTAAGTCCAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTCAATAAACTTGAG 357
Qy 61 LysAlaAspLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 358 AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTGATCGTAAACGCTCCACAGTAACGAC 417
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgGlnGlyLys 100

Db 418 GACTACTTTGAGTCAATTTGATTTTCAAGCGATGCAACCATTTATGATGCAAAACGCGAAG 477
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 478 GTCTACTTTGCTGACAAAGATGGTTCCGTAACCTTCCGACCAACCTGTCCAGNATTT 537
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 538 TTGCTAAGCGCATGTGCGGTTAGACCATATAAAGAAACCAACCAATACAAACCAAGCG 597
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 598 AAATCTGTGTGATGGAATATCTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTTC 657
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 658 AGACGAGTCTCAAGATACCTAAGCTATTGAAACACATAGCTATCGTGACACCATCACA 717
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 718 TCTCAAGATTTACTAGCTCAAGACCAAGCATTTTAAACAAACCAACCCAGGCTATACG 777
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 778 ATTTATGAACGTGACTCTCTCAATCGTCACTCATGACAATGACATTTTCGTCGATTTTA 837
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 838 CCAATGGATCAAGAGTTTACTTACCGTGTAAATAACGGAACAAAGCTTATAGGATCAAT 897
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGlyLysTyrTyr 260
Db 898 AAAAAATCTGCTCTGAATGAAGAAATAAACCAACTGACCTGATCTCTGAGAAATATTAC 957
Qy 261 ValLeuLysLysGlyLysGlyLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 958 GTCTCTTAAAAAAGGGGAAAGCCGTATGATCCCTTTGATCGCAGTCACCTTGAACCTGTTTC 1017
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuTyr 300
Db 1018 ACCATCAAAATACGTTGATGTCGATACCAACGAATTTGTAAGAGTGAGCAGCTCTTTAACA 1077
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1078 GCTAGCGAACGTAACCTTAGACTTCAGAGATTATATACGATCTCTCGTATAGGCTAAACTA 1137
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1138 CTCTACAAACATCTCGATGCTTTTGGTATTATGGACTATACCTTAACCTGGAAGAGTAGAG 1197
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1198 GATAATCAGCATGACACCAACCGTATCATACCGTTTATATGGCAAGCGACCGAAGGA 1257
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1258 GAGAATGCTAGCTATCATTTTAGCC 1281

RESULT 9

US-09-940-235-5
; Sequence 5, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN

```
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-09-940-235-5

Alignment Scores:
Pred. No.: 6.57e-186 Length: 1377
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-5 (1-1377)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 178 AGCCAAATGGTGTGGTACGTTGCTGCTACTGTTGAGGGGAGCAATCAAGACATTAGTCTT 237

Qy 21 LysPheGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 238 AAAATTTTGAATCGATCTAAACATCAGCCTGCTCATGGAGGAGAAAGACAGCAAGGC 297

Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 298 TTAAGTCCAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTCCACATAAATCTTGA 357

Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 358 AAAGCTGACTTACTAAAGGCTTAATCAAGAAATGATCGTACCGTCCACAGTAACGAC 417

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 418 GACTACTTTGAGTTCATGATTTGCAAGCGATGCAACCATTAATGATCGAAACGCAAG 477

Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 478 GTCTACTTTGCTGACAAAGATGGTTGCTGTAACCTTGGCGACCCCAACCTGTCCAAGAATT 537

Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 538 TTGCTAAGCGGACATGTCGCGTTAGACCATATAAAGAAACCAACCAATACAAACCAAGCG 597

Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 598 AAATCTGTTGATGGATATACGTGACGTTTACTCCCTTAACCTGTATGACGATTC 657

Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 658 AGACCAAGTCTCAAGATACCTAAGCTATTGAAACACACTAGCTATCGGTGACCATCACA 717

Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 718 TCTCAAGAAATTTACTAGCTCAAGCAACAAAGCATTTTAAACAAACCAACCCAGGCTATACG 777

Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 778 ATTTATGAGTGACTCTCTCAATGCTCATGACCAATGACATTTTTCGTTACGATTTTA 837

Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 838 CCAATGGATCAAGAGTTTACTTACCGTGTAAATAATCGGGAACCAAGCTTATAGATCAAT 897
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Qy 241 LysLysSerGlyLeuAsnGluGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 260
Db 898 AAAAATCTGGTCTGAATGAAGAAATAAACACACTGACCTGATCTCTGAGAAATATTAC 957

Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
Db 958 GTCCCTTAAAAAAGGGGAAAGCCGATGATCCCTTTGATCGCAGTCACCTTGAACCTGTT 1017

Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLeuLysSerGluGlnLeuLeuThr 300
Db 1018 ACCATCAATACGTTGATGTCATACCAACGAATTTGCTAAAAAGTGAGGAGCTCTTAACA 1077

Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1078 GCTAGCGAAGCTAACTTAGACTTCAGAGATTTATACGATCTCTGATGAAGGCTAAACTA 1137

Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrIleuThrGlyLysValGlu 340
Db 1138 CTCTACAAACAATCTCGATGCTTTTGGTATTATGAGTATATACCTTAACCTGAAAAAGTAGAG 1197

Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1198 GATAATCACGATGACCAACCGTATCATACCGTTTATATGCGCAAGCGACCCGAAGGA 1257

Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1258 GAGATGCTAGCTATCATTTAGCC 1281

RESULT 10
US-10-631-558-5
; Sequence 5, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: Streptococcus equisimilis
US-10-631-558-5

Alignment Scores:
Pred. No.: 6.57e-186 Length: 1377
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-5 (1-1377)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 178 AGCCAAATGGTGTGGTACGTTGCTGCTACTGTTGAGGGGAGCAATCAAGACATTAGTCTT 237

Qy 21 LysPheGluLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 238 AAAATTTTGAATCGATCTAAACATCAGCCTGCTCATGGAGGAGAAAGACAGCAAGGC 297

Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 298 TTAAGTCCAAATCAAAACCACTTTGCTACTGATAGTGGCGGATGTCCACATAAATCTTGA 357

Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 80
Db 358 AAAGCTGACTTACTAAAGGCTTAATCAAGAAATGATCGTACCGTCCACAGTAACGAC 417

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 418 GACTACTTTGAGTTCATGATTTGCAAGCGATGCAACCATTAATGATCGAAACGCAAG 477

Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 478 GTCTACTTTGCTGACAAAGATGGTTGCTGTAACCTTGGCGACCCCAACCTGTCCAAGAATT 537

Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 538 TTGCTAAGCGGACATGTCGCGTTAGACCATATAAAGAAACCAACCAATACAAACCAAGCG 597

Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 598 AAATCTGTTGATGGATATACGTGACGTTTACTCCCTTAACCTGTATGACGATTC 657

Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 658 AGACCAAGTCTCAAGATACCTAAGCTATTGAAACACACTAGCTATCGGTGACCATCACA 717

Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 718 TCTCAAGAAATTTACTAGCTCAAGCAACAAAGCATTTTAAACAAACCAACCCAGGCTATACG 777

Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 778 ATTTATGAGTGACTCTCTCAATGCTCATGACCAATGACATTTTTCGTTACGATTTTA 837

Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 838 CCAATGGATCAAGAGTTTACTTACCGTGTAAATAATCGGGAACCAAGCTTATAGATCAAT 897
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Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 238 AAATTTTTCGAAATCGATTAACATCAGCCTGCTCATGGAGGAAAGACAGACAGGC 297
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 298 TTAAGTCAAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGTCCATATAACTTCAG 357
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsp 80
Db 358 AAAGCTGACTTACTAAAGGCTATTCAAGACAAATTGATCGTAAACGTCACAGTAACGAC 417
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 418 GACTACTTTGAGGTCATTTGTTTGAAGCGATCAACCATTAATGATCGAAGCGCAAG 477
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 478 GTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGGCGACCCCAACCTGTCCAAGAATTT 537
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 538 TTGCTAAGCGGACATGGCGGTTAGACCATATATAAGAAACCAATACAAACCAAGCG 597
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 598 AATCTGTTGATGGATATATCTGTACAGTTTACTCCCTTAACCCCTGATGACGATTC 657
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 658 AGACCAAGTCTCAAGATATACTAAGCTATTGAAACACTAGTATCGGTGACACCATCACA 717
Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 718 TCTCAAGAATTTACTAGCTCAAGCAAAAGCATTTTAAACAAAAACCAACCCAGGCTATACG 777
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 778 ATTTATGAACGTGACTCTCTCAATCGTCACTCATGACCAATGACATTTTCGTACGATTTTA 837
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 838 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGGAACAAAGCTTATAGGATCAAT 897
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 898 AAAAAATCTGGTCTGATGAAGAAATAAACACACTGACCTGATCTCTGAGAAATATTAC 957
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
Db 958 GTCTTTAAAAAGGGGAAAAGCGGTATGATCCCTTTGATCGAGTCACTTGAACACTGTT 1017
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 1018 ACCATCAAAATACGTTGATGTCATACCAACGAATTGCTAAAAAGTGAGCAGCTCTTAACA 1077
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1078 GCTAGCGAAGCTAACTTAGACTTTCAGAGATTTATATACGATCTCTGATGAAGGCTTAAACTA 1137
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1138 CTCTACAAACATCTCGATGCTTTTGGTATTATGACTATATACCTTAATCGGAAAAGTAGAG 1197
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1198 GATAATCAGCATGACACCAACCGTATCATAAACCGTTTATATGGGCAAGCGACCGAAGGA 1257
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1258 GAGAAATGCTAGCTATCATTTTATGACC 1281
```

```
RESULT 11
US-09-471-349-9
; Sequence 9, Application US/094711349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-9
```

```
Alignment Scores:
Pred. No.: 7,57e-186 Length: 1541
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
```

US-09-940-235-2_copy_16_383 (1-368) x US-09-471-349-9 (1-1541)

```
Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 78 AGCCAAATGGGTGTGTAGCGTTGCTGGTACTGTGTAGGGGAGCAATCAAGACATTAAGTCT 137
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 138 AAATTTTTCGAAATCGATTAACATCAGCCTGCTCATGGAGGAAAGACAGACAGGC 197
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 198 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGTCACATAAACTTGAG 257
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsp 80
Db 258 AAAGCTGACTTACTAAAGGCTATTCAAGAAACAAATTGATCGCTAAACGTCACAGTAACGAC 317
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 318 GACTACTTTGAGGTCATTTGATTTTGAAGCGATGCAACCATTAATGATGATGCAACCGCAAG 377
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 378 GTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTTGCCGACCAACCTGTCTCAAGAAATTT 437
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 438 TTGCTAAGCGGACATGTCGCGGTTAGACCATATATAAGAAACCAATCAAAACCAAGCG 497
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 498 AATCTGTTGATGGAAATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
```

```
Db 558 AGACCAGGTCTCAAGATAGTAACTATTGAAACACTAGCTATCGGTGACACCATCACA 617
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 618 TCTCAAGAAATTACTAGCTCAAGCACAAGCAATTTAAACAAAACCCAGGCTATACG 677
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 678 ATTTATGAACGTGACTCTCAATCGTCACTCATGACAATGACATTTTCGCTACGATTTTA 737
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 738 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAACAAGCTTATAGGATCAAT 797
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 798 AAAAAATCTGCTCGAATGAGAATAAACAACACTGACCTGATCCCTTTGATCGAGTATATTAC 857
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLeuPhe 280
Db 858 GTCTCTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGAGTCACTTGAAACTGTTC 917
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 918 ACCATCAAAATACGTTGATGTCGATACCAACGAATTTGCTAAAAAGGTGACGACTCTTAACA 977
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 978 GCTAGCGAACGTAATTAGACTTCAGAGATTTATACGATCTCTCGTGATGAAAGCTAAACTA 1037
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1038 CTCTACAAACATCTCGATGCTTTTGGTATTATGACTATACCTTAACCTGGAAGTAGAG 1097
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1098 GATAATCAGCATGACACCAACCGTATCATACCGTATTATATGGGCAAGCGCCGGAAGGA 1157
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1158 GAGAACTGCTAGCTACCACTTAGCT 1181

RESULT 12
US-09-940-235-9
; Sequence 9, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-9
```

Alignment Scores:

Pred. No.: 7, 57e-186 Length: 1541
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-09-940-235-9 (1-1541)

```
Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 78 AGCCAAATTTGGTTGTAGCGTTCTGCTGTTAGGGGACGAATCAAGACATTAGTCTT 137
Qy 21 LysPheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 138 AAAATTTTGGAAATCGATCTAACATCAGCAGCTGCTCATGGAGGAAAGACAGACGAGC 197
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyValaMetSerHisLysLeuGlu 60
Db 198 TTAAGTCCAAATCAAAACCATTTGCTACTGATAGTGGCGCGATGTCACATAAATTGAG 257
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 258 AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTTGATCGCTAAACGTCACACGTAAC 317
Qy 81 AspTyrPheGluValIleAspPheAlaThrAspAlaThrIleThrAspArgAsnGlyLys 100
Db 318 GACTACTTTTGGTTCATTTGCAAGCGATGCAACCATTTACTGATCGAAACGCGAAG 377
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 378 GTCTACTTTTGTGCAAAAGATGTTTCGGTAACTTTCGCCGACCCCACTGTCCAGAAATTT 437
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 438 TTGCTAACGCGACATGTGCGGTTAGACCATATAAAGAAACCAATAACAAACCAAGCG 497
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspAspPhe 160
Db 498 AAATCTGTTGATGTGGAATATATCTGTACAGTTTACTCCCTTAAACCCCTGATGACGATT 557
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 558 AGACCAGGTCTCAAGATAGTAACTATTGAAACACTAGCTATCGTGACACCATCACA 617
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 618 TCTCAAGAAATTACTAGCTCAAGCACAAGCAATTTAAACAAAACCCAGGCTATACG 677
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 678 ATTTATGAACGTGACTCTCAATCGTCACTCATGACAATGACATTTTCGCTACGATTTTA 737
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 738 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGAACAAGCTTATAGGATCAAT 797
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 798 AAAAAATCTGCTCGAATGAGAATAAACAACACTGACCTGATCTCTGAGAATAATTAC 857
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 858 GTCTCTAAAAAAGGGGAAAAGCCGTATGATCCCTTTGATCGAGTCACTTGAAACGTGTC 917
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 918 ACCATCAAAATACGTTGATGTCGATACCAACGAATTTGCTAAAAAGGTGACGACTCTTAACA 977
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
```

Db 978 GCTAGCGAAGCTAAGCTTACAGAGTTTATACGATCTCTCGTGAAGAGCTAAACTA 1037
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1038 CTCTACAAACAATCTCGATGCTTTTGGTATTATGACCTATACCTTAACCTGGAAGTAGAG 1097
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1098 GATAATCAGCATGACACCAACCGGTATCATACCGTTTATATATGCGCAAGCGCAAGGA 1157
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1158 GAGAATGCTAGCTACCATTTAGCT 1181

RESULT 13
US-10-631-558-9
; Sequence 9, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1541
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-10-631-558-9

Alignment Scores:
Pred. No.: 7,57e-186 Length: 1541
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-2_COPY_16_383 (1-368) x US-10-631-558-9 (1-1541)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 78 AGCCAAATGGTTGTTAGCTTGTCTGCTTACTCTTGGGGGACCAATCAAGACATTAGTCTT 137
Qy 21 LysPheGluIleAspLeuThrSerArgProAlaHisGlyLysThrGluGlnGly 40
Db 138 AAATTTTTTGAATTCGATCTTAACATCAGCCTCTCATGAGGAGAAAGACAGCAAGGC 197
Qy 41 LeuSerProLysSerLysPropheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 198 TTAAGTCAAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGTCAATAAATCTGAG 257
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGlnGluGlnLeuIleAlaAsnValHisSerAsn 80
Db 258 AAAGCTGACTTACTAAAGGCTATTCAAGAAACAATTGATCGCTTAACGTCACAGTAACGAC 317

Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 318 GACTACTTTTGGGTCAATTTGTTTTCGAAGCGATGCAACCATTTACTGATCGAAACGGCAAG 377
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 378 GTCTACTTTGCTGACAAAGATGGTTTCGGTAACCTTTGCGGACCAACCTGCTCCAAAGATTT 437
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 438 TTGCTAAGCGGACATGTGCGGCTTAGACCATATAAGAAACCAACCAATACAAACCAAGCG 497
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 498 AAATCTGTTGATGTGAATATACTGTACAGTTTACTCCCTTAAACCTGATGACGATTTTC 557
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 558 AGACGAGGCTCTCAAGATACCTAAGCTATTGAAACACTAGCTTATCGGTGACACCATCACA 617
Qy 181 SerGlnGluLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 618 TCTCAAGAATTACTAGCTCAAGCAACAAAGCATTTTAAACAAACCAACCCAGGCTAAGC 677
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 678 ATTTATGACGCTGACTCTCTCAATCGTCACTCATGACAATGACATTTTCCGTACGATTTTA 737
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 738 CCAATGGATCAAGAGTTTACTTACCGTGTAAAAATCGGGAACAAGCTTATAGGATCAAT 797
Qy 241 LysLysSerGlyLeuAsnGluIleAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 798 AAAAAATCTGCTGTAATGAAGAAATAAACCACTGACCTGATCTCTGAGAAATATTAC 857
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 858 GTCTTAAAAAAGGGGAAAGCCGTATGATCCCTTTGATCGCAGTCACCTTGAACATGTTTC 917
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 918 ACCATCAATACGTTGATGTCATACCAACGAATTTGCTAAAAAGTCAGCAGCTCTTAAACA 977
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 978 GCTAGCGAAGCTAAGCTTACAGATTTATACGATCTCTCGTGAAGGCTAAACTA 1037
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1038 CTCTACAAACAATCTCGATGCTTTTGGTATTATGACTATACCTTAACCTGGAAGTAGAG 1097
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1098 GATAATCAGCATGACACCAACCGGTATCATACCGTTTATATGCGCAAGCGCAAGGA 1157
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1158 GAGAATGCTAGCTACCATTTAGCT 1181

RESULT 14
US-09-471-349-10
; Sequence 10, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED

; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-10

Alignment Scores:
Pred. No.: 8.31e-186 Length: 1661
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-2_copy_16_383 (1-368) x US-09-471-349-10 (1-1661)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 228 AGCCAAATGGTGTGGTACTGCTGGTACTGCTGGGAGCAATCAAGACATTAGTCTT 287
Qy 21 LysPheGluIleAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 288 AAAATTTTGGAAATCGATCTAAATCAGCACTGCTCATGGAGGAAGACAGCAAGGC 347
Qy 41 LeuSerProTyrSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 348 TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGTCACATAAACTTGA 407
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuLeuAlaAsnValHisSerAsnAsp 80
Db 408 AAAGCTGACTTACTAAAGGCTATTCAAGAAACAATGATCGTAAACGTCACAGTAACGAC 467
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 468 GACTACTTTGAGGTCATGATTTTGCAGCGCATGCAACCATCTGATCGAAACGGCAAG 527
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 528 GTCTACTTTGCTGACAAGATGGTTCGGTAACCTTGGCGACCAACCTGTCCAAGAAATTT 587
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 588 TTGCTAAGCGACATGTGCGGCTTAGACCATATAAAGAAACCAATACAAACCAAGCG 647
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 648 AAATCTGTGATGCGAATATACGTGATGATGATGATGATGATGATGATGATGATGATG 707
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 708 AGACCAGGTCTCAAGATACTAAGCTATTGAAACACTAGCTATCGGTGACCATCA 767
Qy 181 SerGlnGluLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 768 TCTCAAGAAATTAATAGCTCAAGCAAAAGCAATTTTAAACAAAACCAACCCAGGCTATACG 827
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 828 ATTTATGAACGTGCTCTCAATCGTCACTCATGACCAATGACATTTTCCGTACGATTTTA 887
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240

Db 888 CCAATGGATCAAGAGCTTTACTTACCGTGTATAAAATCGGAAACAAGCTTATAGGATCAAT 947
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 948 AAAAATCTGGTCTGAATGAAGAAATAAACAACACTGACCTGATCTCTGAGAAATATTAC 1007
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 1008 GTCCTTAAAAAAGGGGAAAGCCGATGATGATCCCTTTGATCGCAGTCACCTTGAACCTGTC 1067
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 1068 ACCATCAATAGCTTTGATGTCGATACCAACGAATTTGCTAAAAAGTGACGAGCTCTTAACA 1127
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1128 GCTAGCGAACGTAACCTTAGACTTCAGAGATTTATACGATCCCTCGTGAATAGGCTAAACATA 1187
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1188 CTCTACAACATCTCGATGCTTTTGGTATTATGGACTATACCTTAACCTGAAAAAGTAGAG 1247
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1248 GATAATCAGGATGACCAACCGTATCATACCGTTTATATGGCAAGCGACCCGAAGGA 1307
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1308 GAGAAATGCTAGCTATCATTTAGCC 1331

RESULT 15

; Sequence 10, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-10

Alignment Scores:
Pred. No.: 8.31e-186 Length: 1661
Score: 1901.00 Matches: 368
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-2_copy_16_383 (1-368) x US-09-940-235-10 (1-1661)

Qy 1 SerGlnLeuValValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20

Db	228	AGCCAAATGGTGTGTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGACATTAGTCTT	287
Qy	21	LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly	40
Db	288	AAATTTTTGAAATCGATCTAACATCAGCAGCTGCTCATGGAGAAAGACAGCAAGGC	347
Qy	41	LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu	60
Db	348	TTAAGTCCAAATCAAAACCAATTTGCTACTGATAGTGGCGGATGCACATAAACTTGAG	407
Qy	61	LysAlaAspLeuLeuLysAlaIleGlnGlnLeuIleAlaAsnValHisSerAsnAsp	80
Db	408	AAAGCTGACTTACTAAAGGCTATTCAAGAACAAATTGATCGCTAACGTCACAGTAAACGAC	467
Qy	81	AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys	100
Db	468	GACTACTTTGAGGTCATTTGATTTTGCAAGCGATGCAACCACTTACTGATCGAAACGGCAAG	527
Qy	101	ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe	120
Db	528	GTCTACTTTGCTGACAAAGATGGTTCGGTAACCTTGGCGACCCCAACCTGTCCAAGAATTT	587
Qy	121	LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla	140
Db	588	TTGCTAAGCGGACATGTCCGCGTTAGACCATATAAAGAAACCAATACAAAAACCAAGCG	647
Qy	141	LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe	160
Db	648	AAATCTGTGTGATGGAAATATACTGTACAGTTTACTCCCTTAAACCCCTGATGACGATTTT	707
Qy	161	ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr	180
Db	708	AGACCAGGTCTCAAGATACTAAGCTATTGAAACACTAGCTATCGGTGACACCATCACA	767
Qy	181	SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr	200
Db	768	TCTCAAGAAATTAAGTCTCAAGCAACAAAGCATTTAAACAAAAACCCAGCGCTATACG	827
Qy	201	IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu	220
Db	828	ATTTATGAACGTGCTCCTCAATCGTCACTCATGACATGACATTTTCCGTACCGATTTTA	887
Qy	221	ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn	240
Db	888	CCAAATGGATCAAGAGTTTACTTACCGTGTAAATAATCGGGAACAAAGCTTATAGGATCAAT	947
Qy	241	LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr	260
Db	948	AAAAAATCTGCTCTGAATGAAGAAATAAACCAACACTGACCTGATCTCTGAGAAATATTAC	1007
Qy	261	ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe	280
Db	1008	GTCCCTTAAAAAGGGGAAAAACCGTATGATCCCTTTGATCGCAGTCACCTTGAAACTGTTC	1067
Qy	281	ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr	300
Db	1068	ACCATCAAAATACGTTGATGTGATACCAAGAAATGCTTAAANAGTGACAGCTCTTAAACA	1127
Qy	301	AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu	320
Db	1128	GCTAGCGAAGTAACTTAGACTTCAGAGATTTATACGATCTCTCGTGATAAGGCTAAACTA	1187
Qy	321	LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu	340
Db	1188	CTCTACAAACAATCTCGATGCTTTTGGTATTATGACACTATACCTTAACTGGAAAAAGTAGAG	1247
Qy	341	AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly	360
Db	1248	GATAATCACGATGACACCACCGTATCATACCCGTTTATATGGGCAAGCCGCAAGGA	1307
Qy	361	GluAsnAlaSerTyrHisLeuAla	368

Search completed: November 6, 2004, 07:38:35
Job time : 6049.11 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:38:12 ; Search time 114.055 Seconds
(without alignments)
747.335 Million cell updates/sec

Title: US-09-940-235-2_COPY_16_383

Perfect score: 1901

Sequence: 1 SQLVSVAGTVEGTNQDISL.....IITVMGKRPGENASYHLA 368

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delpop 6.0 , Delpext 7.0

Searched: 63957 seqs, 115811272 residues

Total number of hits satisfying chosen parameters: 1387914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09940235/runat_03112004_174040_11339/app_query.fasta_1.1045
-DB=Pending_Patents_NA_New -QFMT=fastap -SUFFIX=p2n.rnpn -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40 cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09940235 @CGN_1_1.480 @runat_03112004_174040_11339
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending_Patents_NA_New.*

- 1: /cgn2_6/ptodata/2/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/2/pna/US06_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/2/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/2/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/2/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/2/pna/US11_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/2/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1432	75.3	1299	8	US-60-615-573-2546 Sequence 2546, Ap
2	1403	73.8	1323	8	US-60-615-573-2545 Sequence 2545, Ap
3	1369	72.0	1323	8	US-60-615-573-2544 Sequence 2544, Ap
4	125.5	6.6	1344	8	US-60-615-573-7001 Sequence 7001, Ap
5	124	6.5	1343	8	US-60-615-573-7002 Sequence 7002, Ap
6	109.5	5.8	1512	8	US-60-615-573-18391 Sequence 18391, A
7	107.5	5.7	6806	6	US-10-956-160-1475 Sequence 1475, Ap
8	105	5.5	3859	6	US-10-163-587B-3 Sequence 3, Appli
9	104.5	5.5	1248	8	US-60-615-573-13062 Sequence 13062, A
10	102	5.4	2697	8	US-60-615-573-7856 Sequence 7856, Ap

11	101.5	5.3	266145	6	US-10-856-118-1	Sequence 1, Appli
12	100.5	5.3	945	8	US-60-615-573-12450	Sequence 12450, A
13	100	5.3	1584	6	US-10-956-157-943	Sequence 943, App
14	100	5.3	3845	6	US-10-163-587B-5	Sequence 5, Appli
15	99.5	5.2	1860	8	US-60-615-573-7919	Sequence 7919, Ap
16	98	5.2	1012	8	US-60-615-573-1845	Sequence 1845, Ap
17	97.5	5.1	2682	8	US-60-615-573-14432	Sequence 14432, A
18	96	5.0	2000	8	US-60-615-573-18494	Sequence 18494, A
19	96	5.0	3093	8	US-60-615-573-17425	Sequence 17425, A
20	95.5	5.0	2140	6	US-10-510-386-75	Sequence 75, Appli
21	95.5	5.0	2568	8	US-60-615-573-12512	Sequence 12512, A
22	95.5	5.0	7888	6	US-10-956-157-1031	Sequence 1031, Ap
23	94.5	5.0	2214	8	US-60-615-573-14190	Sequence 14190, A
24	94.5	5.0	266145	6	US-10-856-118-1	Sequence 1, Appli
25	94	4.9	1284	8	US-60-615-573-17277	Sequence 17277, A
26	94	4.9	1860	8	US-60-615-573-18498	Sequence 18498, A
27	94	4.9	7145	8	US-10-956-160-667	Sequence 667, App
28	94	4.9	30612	8	US-60-620-788-64	Sequence 64, Appl
29	93.5	4.9	2028	8	US-60-615-573-14199	Sequence 14199, A
30	93	4.9	1836	8	US-60-615-573-12429	Sequence 12429, A
31	92.5	4.9	1509	8	US-60-615-573-7338	Sequence 7338, Ap
32	92.5	4.9	3012	8	US-60-615-573-7892	Sequence 7892, Ap
33	92	4.8	1632	8	US-60-615-573-9954	Sequence 9954, Ap
34	92	4.8	2604	8	US-60-615-573-14424	Sequence 14424, A
35	91.5	4.8	726	6	US-10-663-094-32	Sequence 32, Appl
36	91	4.8	1227	8	US-60-615-573-7848	Sequence 7848, Ap
37	91	4.8	1731	8	US-60-615-573-819	Sequence 819, App
38	91	4.8	1998	8	US-60-615-573-18415	Sequence 18415, A
39	91	4.8	6319	6	US-10-956-157-708	Sequence 708, App
40	91	4.8	140680	6	US-10-746-294A-83	Sequence 83, Appl
41	90.5	4.8	700	6	US-10-956-157-1731	Sequence 1731, Ap
42	90.5	4.8	700	6	US-10-956-157-6966	Sequence 6966, Ap
43	90.5	4.8	741	6	US-10-734-049A-384	Sequence 384, App
44	90.5	4.8	1400	6	US-10-956-157-6178	Sequence 6178, Ap
45	90	4.7	2457	8	US-60-615-573-13084	Sequence 13084, A

ALIGNMENTS

RESULT 1
US-60-615-573-2546
; Sequence 2546, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2546
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (597)..(597)
; OTHER INFORMATION: n is a, c, g, or t
US-60-615-573-2546

Alignment Scores:	7,918-161	Length:	1299
Pred. No.:	1432.00	Matches:	290
Score:	82.61%	Conservative:	14
Percent Similarity:	78.88%	Mismatches:	56
Best local Similarity:	75.33%	Indels:	8
Query Match:	8	Gaps:	1
DB:			
US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-2546 (1-1299)			


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Qy 1 SerGlnLeuValSerValalaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 124 AGCCAAATTAGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGAAATTAGCCTT 183
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 184 AAAATTTTGAATTTGAAATGACCTAACATCAGCAGCTGCTCAGGGAGGAAACAGACGACGCGC 243
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 244 TTAGCTCAAAATCAAAA-----ATGCCATATAAACTGAA 279
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 280 AAAGCTGACTTATTAAAGGCTATTCAAGAACAAATGATCGCTAACGTTTCACAGTAACGAC 339
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 340 GGCTACTTTGAGGTCAATTGATTTTGCAGAGCATGCAACCATCCTGATCGAAACGGCAAG 399
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 400 GTCTACTTTGCTGATCGAGATGATTGCGTAACCTTGGCCGACCAACCTGTCCAGAATTT 459
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 460 TTGCTAAGCGGCGATGTGCGGCTTAGACCGTATCRMCCATARCCGTTTCACAACTCGCT 519
Qy 141 LysSerValAspValGluThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 520 GAACGCGRTTAAACGTCACATGAGTGAAGTGTGCTCCGAAACAGGAGARATTTAGACTTT 579
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 580 ACRCMTVTGTTAARANCRATATACATTTGACCACACTGGCGAGTTGGTGACTCTCTTTCA 639
Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 640 TCACAAGAGTTAGCAGCATTGCCCCAATTTATCTATCAAAARARYATCCAGATTAATC 699
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 700 ATTACAAACCKGACTCTCTCAATGCTCAATGCTCAACATGACAAKAGAYATTTCCGTACGATTTA 759
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 760 CCAATGGATCAAGAGTTTACTTACCRTRYAAARAYCGGGAACAGCTTATGGGRTCAAT 819
Qy 241 LysLysSerGlyLeuAsnGluLeuIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 820 AAAAAATCTGTCAGRWGRAAAATRAACAACACACACCTCATCTCTGAGAAATATTAY 879
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 880 RTCTCTAAAAAAGGGARRAGCKYRTRATCCCTTTGATCGCAGTCACTTGAACACTGTTC 939
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 940 ACCATCAATTACGTTGATGTGCATACCAACAAATTTGCTAAAAAGCGACGACTCTTAACA 999
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1000 GCTAGCGNACGTAACCTAGACTTCAGAGATTTATACGATCTCTGATAGGCTTAACCTA 1059
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1060 CTCTACACAATCTCGATGCTTTTGGTATTATGACTATACCTTAACCTGGAAGAGTAGAG 1119
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1120 GATAATCACGATGACACCAACCGTATCATACCGTTTATATATGGGCAAGCGACCCGAGGA 1179
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
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Db 1180 GAGAATGCTAGCTATCATTTAGCT 1203
RESULT 2
US-60-615-573-2545
; Sequence 2545, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2545
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (621)..(621)
; OTHER INFORMATION: n is a, c, g, or t
US-60-615-573-2545
Alignment Scores:
Pred. No.: 2,3e-157 Length: 1323
Score: 1403.00 Matches: 283
Percent Similarity: 79.62% Conservative: 10
Best Local Similarity: 76.90% Mismatches: 75
Query Match: 73.80% Indels: 0
DB: 8 Gaps: 0
US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-2545 (1-1323)
Qy 1 SerGlnLeuValSerValalaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 124 AGCCAAATTAGTTGTTAGCGTTGCTGGTACTGTTGAGGGGACGAATCAAGAAATTAGCCTT 183
Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyThrGluGlnGly 40
Db 184 AAAATTTTGAATTTGAAATGACCTAACATCAGCAGCTGCTCABGGAGGAGAAACAGACGACGACG 243
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 244 TTAMRTCCAAATCAAAACCAATTTGCTACAGATAAAGGCGCAATGYCACATAAACTTGAA 303
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 304 AAAGCTGACTTATTAAAGGCTATTCAAGAACAAATTTGTCGCTAACGTTTCACAGTAACGAC 363
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 364 GGCTACTTTGAGGTCAATTGATTTTGCAGAGCATGCAACCATVACTGATCGAAACGGCAAG 423
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 424 RTCTACTTTGCTGAYMRAGATGATTGCGTAAATTTGCGCGACCAACCTGTCCAAGAAATTT 483
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 484 TTGCTAAAGGGGCGATGCGCGTTTARCCGTTATCRMCCATCRMCCGTTTCAACTCWGCT 543
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 544 RAACGCGTTTAACRTCAACTATGAGTGGCTTTGCTCCGAAACAGGAGATTTTAGACTTT 603
Qy 161 ArgProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 604 ACRCRTYGTTAARANCRATATYCAVTTTGASACACTRGCRGTGGTGACTCTCTTTCA 663
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Qy 181 SerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 664 TCACARAGATTGACGACGATTTGCTTATCAAAARARATCCGATTATATC 723
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 724 ATTACAAAGCGTACTCTCAATCGTCACATCAAGCAAGATTTTCCGACGATTTTA 783
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 784 CCAAYGGATCAAGAGTTTACTTACCTRTTYAARAYCGGGACCAAGCTTATRGBCAAT 843
Qy 241 LysLysSerGlyLeuAsnGluGluLeuAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 844 HMWAAACWGRMTMKRWGDAARAYRAAACAACACACACCTCATVCTCGAAGAAATATTAC 903
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 904 RTCCTTAAAGGARRAGCGGTATATCCCTTKGATCGCAGTCACTTGAAACTGTTC 963
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 964 ACCATCAATACGTGATGTCRAVACCAASRWMTTGCTTAAAGCGGACGACTCTTAACA 1023
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1024 GCTAGCGAACRTAACTTAGACTTCAGAGATTATACGATCTCTGATAGAGCTTAACTA 1083
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1084 CTCTACAAACAATCTCGATGCTTTGGTATTATGTCGCTATACCTTAACTGGAAAGTTCAG 1143
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1144 GATAATCAGATGACACCAACCGGTATCATACCGTTTATATGGCAAGCGACCCGAAAGG 1203
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1204 GAGAAATGCTAGTATCATTTAGCY 1227
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RESULT 3

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US-60-615-573-2544
; Sequence 2544, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2544
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Streptococcus pyogenes
US-60-615-573-2544
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Alignment Scores:
Pred. No.: 2,57e-153 Length: 1323
Score: 1369.00 Matches: 278
Percent Similarity: 77.17% Conservative: 6
Best Local Similarity: 75.54% Mismatches: 84
Query Match: 72.01% Indels: 0
DB: 8 Gaps: 0
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US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-2544 (1-1323)

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Qy 1 SerGlnLeuValSerValAlaGlyThrValGluGlyThrAsnGlnAspIleSerLeu 20
Db 124 AGCCARTTAGTTGTAKGTATGGCGGTATCGTTGAAAGTACCGATATAAAGATTTTATA 183
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Qy 21 LysPhePheGluIleAspLeuThrSerArgProAlaHisGlyGlyLysThrGluGlnGly 40
Db 184 AATTTTTTTGAAATCGATCTAATCAACACACACACACACACACACACACACACACAC 243
Qy 41 LeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGlu 60
Db 244 TTAAGTCACAAATCAAAATTTCTTACATATATRGCGCATGCCACATAAATTTGAA 303
Qy 61 LysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAsp 80
Db 304 AAAGCTGACTTATTAAAGCTATTCAARAACGCTGATCGCTAACCTYCACAGTAAYGAC 363
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 364 GGCTACTTTGAGTGTATTTGCAAGCGATGCAACCATTTACTGAYCGMRACGRYMAS 423
Qy 101 ValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPhe 120
Db 424 RTMTACTTTGCTTTRRYMAAGATGRTYTCGGTAACTTTGCCSACCACCTCTTCCAASATTT 483
Qy 121 LeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAla 140
Db 484 TTGTFWAVVGRKATGTTCGCGTTAGACCATATAAGAAACCAACARTACAAATWCAGCR 543
Qy 141 LysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPhe 160
Db 544 ARATCTGYGATRRERRATATCTGTACAGTTTACCTTTCCTTAAACCTGATGAYGATTTC 603
Qy 161 ArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIleGlyAspThrIleThr 180
Db 604 AVRCMGKKMTCAAAARRTACTTAARCTATTGAAAMAYTAGCTATCGGYRRCCRTCCACA 663
Qy 181 SerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThr 200
Db 664 TCYCAAGAATTTACTAGCTCAAGCAACAAAGCATTTTAAWCRAAASCCAYTCARRYATACG 723
Qy 201 IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 724 ATTATGACGTGATTCCTCAATCGTACTCATNGACRAKGRYATTTTCGTACRATTTTA 783
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 784 CCAAYRGATCAARAGTTTACTTACCTRTTYAARAYCGGAAACAAAGCTTATVRRRHCRAY 843
Qy 241 LysLysSerGlyLeuAsnGluGluLeuAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 844 HMWAAACWGRMTMKRWARARAYDAAMAACACACACACCTCTCTCGAGAAATATTAC 903
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 904 RTCCTTAAAMAARGGARDMKCCGATGATCCCTTTGATCGCAGTCACTTGAACATGTTTC 963
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 964 ACCATCAATAGTTGATGTCRAYACCAASRWMTTCTTAAAGGAGGAGAGCTCTTAACA 1023
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 1024 GCTAGCGAASGTAACCTTAGACTTCAGAGATTATACGATCCCTYGTGATAGGCTAAACTA 1083
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu 340
Db 1084 CTCTACAAACAATCTGTGCTTTGRTATYATGACTATACCTTTAACTCGAAGTAGAG 1143
Qy 341 AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly 360
Db 1144 GATAATCAGATRASAMYAYCGTTRTYTHACMGTTTATATGGGYAAGCGMCCYRAAGR 1203
Qy 361 GluAsnAlaSerTyrHisLeuAla 368
Db 1204 GMRAAKGSTAGCTATCATTTAGCY 1227
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Db 142 ATTATTGTAATGTTACAGGTACTGATCAAAACCGGAAT---AGCATTTTACCGCATTTAT 198
Qy 23 PheGluIleAspLeuThrSerArgProAlaHisGlyGlyLeuThrGluGlnGlyLeuSer 42
Db 199 ATCGAAGTCAATGTA----- 213
Qy 43 ProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeuGluLysAla 62
Db 214 -----AAGATGGGACAAACTTTAAGTAAARAA 240
Qy 63 AspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnVal-----HisSerAsnAsp 80
Db 241 GAAATTCAGATTATATTCCTCGAAATTTAAACTCTAGTGTGGAGGACAAAGTAAACAA 300
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAla-----ThrIleThrAsp 96
Db 301 GTTCAATACCAACATCGAGTTTAAGAAAGTCTTATCTGAACGCTCAATTAGATGAT 360
Qy 97 ArgAsnGlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnPro 116
Db 361 GGCAAGACAGAGAAATAGCAATTGATAACGACGCT---GTTACTGTACCTAAAGACGGT 417
Qy 117 ValGlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIle 136
Db 418 CCAACAAATTTTGGATTGACGTTCCAGTAACCTTGTACGGTAAATTTCAATAACTCCAAAG 477
Qy 137 GlnAsnGlnAlaLys-----SerValAspValGluTyrThrValGlnPheThrPro 153
Db 478 CTCCATAAGTAGAATGGGGTACACTATTTTCAGTTTACATTTATGATGACGTTGTT--- 534
Qy 154 LeuAsnProAspAspAspPheArgProGlyLeuLysAspThrLysLeuLeuLysThrLeu 173
Db 535 -----GATAAACTACAGGTAAACTTTAGAGGATTTTAAACTATTGATTTTCT 585
Qy 174 AlaIle-----GlyAspThrIleThrSerGlnGluLeuLeuAla 186
Db 586 GAAATCGACCTTGGAAATTCGACATACCGGTGATAGCATTACCGATAGGAAGTATATAAC 645
Qy 187 GlnAlaGlnSerIleLeuAsnLysAsn-----HisProGlyTyrThrIleTyrGlu 203
Db 646 TCAGCTTACAGTGCTTTTAAAGSAGTAAATTAATAAGCAAGGYATTCAATTTCCAATAC 705
Qy 204 ArgAspSerSerIleValThrHisAsnAspIlePheArgThrIleLeuProMetAsp 223
Db 706 AGAATTAGTACAGATGTTCAACAAATCTTCAAGTCACCAAAACTTTCAACTACGAT 765
Qy 224 -----GlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 766 GTAAATGAAGAAATTGATTAACTATCAAAATCGAAACAAATAGACCCACACTAAACCTATCT 825
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyr 260
Db 826 AATRAAGCC-----GAGACTGATATCTTTTCGAAAGATATTAT 864
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 865 GTTTCTAGATGGA-----GATAGTTTACACGCTACAGAA---TCAACWATT 909
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSerGluGlnLeuLeuThr 300
Db 910 TCGATTAAATGGTTGATGCCAAACTCAAAACGCTATTTTAACCCACACATTAACGGGT 969
Qy 301 AlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu 320
Db 970 -----TATASACATTGKCAACT-GTTTCCAAT 995
Qy 321 LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLys----- 338
Db 996 GTCTATACAGACTCTTTGAAGAAATCTTATCCCAACTCAAAATCAGGAGAAARATAT 1055
Qy 339 ---ValGluAspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArg 357
Db 1056 TTTATTCAAAATATGAAAAAACAGCTGAACAAGAATATACTGTTTACCITTCAGAAACA 1115
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Qy 358 ProGluGlyGlu 361
Db 1116 CCTTATTCTGAA 1127
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RESULT 6

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US-60-615-573-18391
; Sequence 18391, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18391
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-60-615-573-18391
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Alignment Scores:
Pred. No.: 0.0027 Length: 1512
Score: 109.50 Matches: 74
Percent Similarity: 34.45% Conservative: 45
Best Local Similarity: 21.45% Mismatches: 123
Query Match: 5.76% Indels: 103
DB: 8 Gaps: 15
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US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-18391 (1-1512)

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Qy 48 PheAlaThrAspSerGlyAlaMetSer---HisLysLeuGluLysAlaAspLeuLys 66
Db 487 TATTACACTCTCGAAGGTACTATAAAGTTCCAAAAATTTTAAATCCAGAACTTGAANAAT 546
Qy 67 AlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsnAspTyrPhe----- 83
Db 547 TCACAAATCACAACTTATTATTATTAACACCGGATTTCAACTTAAGTATTTAATAATGAT 606
Qy 84 ---GluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLysValTyr 102
Db 607 CAGGAATTACTAGCATTTGCAATTCGAAAAATTTGTAT-----AAAAATCGAGATATTTTC 660
Qy 103 PheAlaAspLysAspGlySerVal-----ThrLeuProThrGlnPro 116
Db 661 CTGAGTGATAAAATATAAATACTCCACCAATATTCAATAATACTAGTGAACAAATACCT 720
Qy 117 ValGlnGluPheLeuLeuSerGlyHisVal---ArgValArgProTyrLysGlyLysPro 135
Db 721 GTTTTAGCTGTTTGCATAGTACTCATGTCWAGAATATTGACATGATATGATGAATCGGAC 780
Qy 136 IleGlnAsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsn 155
Db 781 ATCAAAAATACTTTAAACATGTT-----TTTAACAATCTTAAAT 819
Qy 156 ProAspAspAspPheArgProGlyLeuLysAspThrLysLeuLysThrLeuAlaIle 175
Db 820 AGATACTCT----- 828
Qy 176 GlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsn 195
Db 829 GGGATAATTGTCGACTAAACCAACAAATTTGGATATATATCAGCTCGAATAAATAATGAA 898
Qy 196 HisProGlyTyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIle 215
Db 889 ATCCCTGTTCACTACTATA----- 906
Qy 216 PheArgThrIleLeuProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGln 235
```

Db		907	- - - - CCACTAGATATAATTGATGAACAATTTACTAATTTAAAGAAGAAAT-	-----	951
Qy	.	236	AlaTyrArgIleAsnLysSerGlyLeuAsnGluGlutIleAsnAsnThrAspLeuIle	255	
Db		952	-- -- -- -- AATCATAGTAGTAATAATAATAAAAAATTTATT	981	
Qy		256	SerGluLysTyrTyrrValLeuLysLysGly- - - - - GluLys	267	
Db		982	TCCGTGGCAGTTATTCCTCGAAAACAGTGGAATCAAATGGAATTTAGTTCTTAA	1041	
Qy		268	ProTyrAspProPheAspArgSerHisLeuLysLeuPheThrIle- - - - -	282	
Db		1042	TTAATTAAGAAGAAATTTCCCTAACATCCRACTACATTTGTATGGTTTGCATAAGAAGAGAA	1101	
Qy		283	LysTyrValAspValaspThrAsnGluLeuLysSerGluGlnLeuLeuThrAlaSer	302	
Db		1102	AAATACAAAGCAACTAATCACTCGAATATAATTTTTAGAAAACAATGTGTTTTTACGAGGGTTT	1161	
Qy		303	GluArgAsnLeu- - - AspPheArgAspLeuTyrAspProArgAspLysAlaLysLeu	320	
Db		1162	AGAAGAAATTTAAGTGTGTGAGATTCAAGATGCTTAT- - - - - ATGCTCTTA	1206	
Qy		321	LeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeuThrGlyLysValGlu	340	
Db		1207	ATTACTAGTAAATATGGAAGGATTTAAATTTA- - - - GGTTTATTAGAA	1248	
Qy		341	AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly	360	
Db		1249	- - - - - ACTATACTAGAGCATACCCTCCAGTTGGC	1278	
Qy		361	GluAsnAlaSerTyr	365	
Db		1279	TATAAATTCGAAGTAT	1293	

```

RESULT 7
US-10-956-160-1475
; Sequence 1475, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956,160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1475
; LENGTH: 6806
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-1475

```

Alignment Scores:	
Pred. No.:	0.0426
Score:	107.50
Percent Similarity:	31.52%
Best Local Similarity:	16.28%
Query Match:	5.65%
DB:	6
Gaps:	14
Indels:	147
Mismatches:	118
Conservative:	59
Matches:	63
Length:	6806

US-09-940-235-2 COPY 16 383 (1-368) x US-10-956-160-1475 (1-6806)

Qy	33	HisGlyGlyLysThr	-----GluGlnGlyLeuSerProLysSer	45
		:::	:::	
Db	904	CATTCTGTCGATCATGATAGACCTCCCGGCACACGGTCACCGTCACTTCAGCAA	963	
		:::	:::	
Qy	46	LysProPhealathrAspSerGlyAlaMetSerHisLysLeuGluLysAlaAspLeuLeu	65	
		:::	:::	
Db	964	CGATCAGAGCCTTCTGATCATTCAGACACTCTCCACAGCAGCCACGATGGCAGTCTC	1023	
		:::	:::	
Qy	66	LysAlaIleGlnGluGlnLeuIleAlaAsn	-----ValHis	77
		:::	:::	

1024	CGAGCAGACAGAGAGAGAAATTTCTAAACCTGGGGCTGTCTCAACTCCTCTGAAGCAT	108
78	SerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArg	97
1084	CGAGATGTCATACACATAAAACAGTA-----GAAGAAGTTGTAGTTGAGAGA	1131
98	AsnGlyIysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProVal	117
1132	AATGAGAAA-----CAAGCACCCAGTCTTCCA-----	1158
118	GlnGluPheLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGln	137
1159	-----GAACAAAGCCTCTGTAT	1176
138	AsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAsp	157
1177	GCTCAAGTTGGCAACACAGATGGAT-----TTACTCTGTCACTCCATCT	1221
158	AspAsp-----PheArgProGlyLeuLysAsp	166
1222	GATGGCGTCTACCTAATTCAACTCATGAAGTGGGATTTCTCCGGCCACGATGAATTC	1281
167	ThrLysLeuLeuLysThrLeuAlaIleGly-----	176
1282	GTAAATTCAGAAAGAGAGATAGTGTGGCTCGCTCGCTGGTGGAAATGATGTTGGA	1341
177	-----AspThrIleThrSerGlnGluLeuAlaGlnAla	188
1342	ATATTTCTAGCTGGTGTCTAGAAGATAGCCCTGCAGCCAAAGAGCTTTAGAAGAGGT	1401
189	GlnSerIleLeuAsnLysAsnHisProGlyTyrThrIleTyrGluArgAspSerSerIle	208
1402	GATCAAAATTTCTAGGGGTAAACAATGTAGATTTTCACA-----AACATC	1443
209	ValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGluPheThrTyr	228
1444	ATAAGAGAAGACCGCTTTTCTCTCGACTCCCTAAAGGAGAAGATGACCATTA	1503
229	ArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGlu	248
1504	TTGGCTCAGAAAGAAAGATGTTTATCGT-----CGC	1536
249	IleAsnAsnThrAspLeuLeuSerGluLysTyrTyrValleuLysLysGlyGluLysPro	268
1537	ATTGTAGATCAGAT--GTGGGAGATCTTTCTATATT-----	1572
269	TyrAspProPheAspArgSerHisLeuLysLeuPheThrIleLysTyrValAspValAsp	288
1573	-----AGAACCCTTTGAA-----	1587
289	ThrAsnGluLeuLysSerGluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPhe	308
1587	-----	1587
309	ArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPhe	328
1588	-----TATCAAAAGGAATCTCCCTACGGACTTAGTTTAAACAAAGAGAGGTGTTT	1638
329	GlyIleMetAspTyrThrLeuThrGlyLys-----ValGlu	340
1639	CGTGTGTGGATACCTTGTACAAATGGGAACATAGGCTCTGGCTCGCTATTCGAATGGC	1698
341	AspAsnHisAspAspThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGly	360
1699	AAAATCATAAAGAGTAGAACAGGCAATCATCCCTAATAAGAACAGGGCTGACGAGTTA	1758
361	GluAsnAlaSerTyrHisLeu	367
1759	GCCAGTGTACAGTACACACTT	1779

RESULT 8

US-10-163-587B-3

Sequence 3, Application US/10163587B

GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163.587B
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/296,110
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 3859
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (160)..(3204)
US-10-163-587B-3

Alignment Scores:

Pred. No.: 0.0367 Length: 3859
Score: 105.00 Matches: 84
Percent Similarity: 35.66% Conservative: 49
Best Local Similarity: 22.52% Mismatches: 114
Query Match: 5.52% Indels: 127
DB: 6 Gaps: 16

US-09-940-235-2_COPY_16_383 (1-368) x US-10-163-587B-3 (1-3859)

Qy 35 GlyLysThrGluGlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGly-Al 54
Db 1648 GGGAGTCAGCGGCTCGCTCTCCAAAAGAGCAAGCGCCAGGTCAAGAGGAGGTATC 1707
Qy 54 aMetSerHisLysLeuGluLysAlaAspLeuLysAlaLeGlnGluLeuLeuAl 74
Db 1708 AACAAATCTGAAAGAGAGAAATTAACCTTAAAG-----GAGGAGCAGCTG- 1756
Qy 74 aasnValHisSerAsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrI 94
Db 1757 -----TGATCTCTGATTTCTGGAGTGGAA-CACCTCTGCGCATGT 1793
Qy 94 eThrAspArgAsnGlyLysValTyrPheAla- 104
Db 1794 CCTGGAGAAAGTGGGAGGTCTTCAGTGCACCCCTGGCTGGTGGACATCGTTAAAG 1853
Qy 105 -----AspLysAsp 107
Db 1854 AACCAACTCTACTACAAGCTGCAGCTTCTGGAGGAGCAGCAAGGAAACACAGTATTGGAT 1913
Qy 108 -----GlySerValThrLeuProThrGlnPr 116
Db 1914 ATTCAGTCTCTGGGCGGTGTGGGTACGGTGATCGGTAGCAACAACTGGAACAGATGCC 1973
Qy 116 oValGlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProI 136
Db 1974 GTCCAGGAGATGCCATGAGCATGATCAATA-----TATGAAGAAACACCGG 2027
Qy 136 eGlnAsnGlnAlaLysSerValAspValGluTyrThrValGlnPheThrProLeuAsnPr 156
Db 2028 GAACGCTTGGCACTCCAAAATTTTCAGAGTATCCCAAAAGTTTACCCCTGGAGAT 2087
Qy 156 oAsp-----AspAsp 165
Db 2088 TGACTATGGCAGGATGAAGAGCGCAGTGAAGAGCTCACAGTAAATCTCGGCACCAAGTC 2147
Qy 166 -----AspThrLysLeuLeu 171
Db 2148 CAAGCTCCCAAGCAGTTCAGGACCTCATCAAGATGATCTTTGATGGAAAGTATGAA 2207
Qy 171 sThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeu 184
Db 2208 GAAAGCATGGTGGAGTATGATGATCGACCTTCAGAGATGCCCTTGGGAAGCTGAGCAA 2267

Qy 185 -----LeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThrIle 202
Db 2268 AAGCAGATCCAGCGCGCATCTCCATCTCAGTGAGTCCAGCAGCGGTCTCAGCG 2327
Qy 202 rGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIleLeuProMe 222
Db 2328 CAGCAGCGACTCTCAGATCTCTCAAAATCGC-----TTTACACCTGATCCGCCA 2384
Qy 222 tAspGlnGluPheThrTyrArgValIysAsnArgGluGlnAlaTyrArgIleAsnLys 242
Db 2385 CGACTTTGGGATG-----AAGAA 2402
Qy 242 sSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLys----- 258
Db 2403 GCCTCCGCTC-----CTGAACAATCCACAGACAGTGTGAGGCCCAAGTGAATGCT 2453
Qy 259 -----TyrTyrValLeuLysLysGly-----Glu 267
Db 2454 TGACAACCTGCTGGACATCGAGGTGGCTTACAGTCTGCTCAGGGAGGCTCTGATGATAG 2513
Qy 267 sProTyrAspProPheAspArgSerHisLeuLysLeuPheThr-----IleLysTyrValAs 286
Db 2514 CAGCAAGGATCCCATCGATGTCAACTATGAGAAGCTCAAACTGACATTAAGGTGTTGA 2573
Qy 286 pValAspThrAsnGlu-----LeuLeuLysSerGluGlnLeuLeuTh 300
Db 2574 CAGAGATCTGAAGAGCGGAGATCATCAGGAGTATGTGAAGACTCATGATCATGCAACCAC 2633
Qy 300 rAlaSerGluArgAsnLeuAspPheArgAspLeuTyr 312
Db 2634 ACACAGTCCGTATGACTTGGAGTATCGATATCTTT 2670

RESULT 9

US-60-615-573-13062
; Sequence 13062, Application US/60615573
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13062
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-13062

Alignment Scores:

Pred. No.: 0.00801 Length: 1248
Score: 104.50 Matches: 71
Percent Similarity: 37.13% Conservative: 53
Best Local Similarity: 21.26% Mismatches: 125
Query Match: 5.50% Indels: 85
DB: 8 Gaps: 16

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-13062 (1-1248)

Qy 58 LysLeuGluLysAlaAspLeuLeu-----LysAlaIleGlnGluGln 71
Db 274 AAAATAATAAGGAGATAAAGTTTCAATTTTAAATCAAAAGTAAAGTATTAACAATGAA 333
Qy 72 LeuIleAlaAsnValHisSerAsnAspTyrPheGluValIleAspPheAlaSerAsp 91
Db 334 CCAATTAAGTATTAATTCAGTATGATTTTCAAAATGTTGTTGATTT 384
Qy 92 AlaThrIleThrAspArgAsnGlyLysValTyrPheAlaAspLysAspGlySerValThr 111

Db 385 -----GATAAAATGTAAGAGTCTTTATCCCTAAAGATGAACACTACTGTTTCAT 432
Qy 112 LeuProThrGlnProValGlnGluPhe-----LeuLeuSerGlyHisValArgVal 128
Db 433 GATTCATTAATTTCAAGAGATTTTAAACAATGTGACAAACACAGGGTGTTACTAAAGTA 492
Qy 129 ArgProTyrLysGlu-----LysProIleGlnAsnGlnAlaLys 141
Db 493 AACGAAGATAATGAAGTTTCGAATGGATAGCAAAATCAATCTCTAATGAATTTAGTGTAA 552
Qy 142 SerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAspPheArg 161
Db 553 ACGCTT-----TATTAGTTGTAAAGAGAACAACTAAAGAAAGATGCTGATTATAAA 603
Qy 162 ProGlyLeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThr----- 178
Db 604 AAATATATTAGTGAT-----AACTTACATCAATTTCTGATGTAGCTAAAGAA 651
Qy 179 ---IleThrSerGlnGlnLeuLeuAlaGlnSerIleLeu----- 192
Db 652 CAATTAATTCACAGAGCTCACGCTCAACAGTGTAGATGTGATTATTAAGCCAGACTCA 711
Qy 193 AsnLysAsn-----HisProGlyTyrThr----- 200
Db 712 AACAAAGAACCTTGATTATTATACAAATGCTTTAGCACATCAACACATTAGTTTATGATTTA 771
Qy 201 IleTyrGluArgAspSerIleValThrHisAspAsnAspIlePheArgThrIleLeu 220
Db 772 TTGAATGATAGAAAATAAAAAAGCAACAATATAAATCAATCAACAACT----- 825
Qy 221 ProMetAspGlnGluPheThrTyrArgValLysAsnArgGluGlnAlaTyrArgIleAsn 240
Db 826 -----TCTAGTAGCTAAAGATATTCAAAATTCACAAAC 861
Qy 241 LysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSerGluLysTyrTyr 260
Db 862 AAGTAAAGTAATTCGAATATAAATA---ACATTGAATATTACAAGTGTAGTATGAA 918
Qy 261 ValLeuLysLysGlyGluLysProTyrAspProPheAspArgSerHisLeuLysLeuPhe 280
Db 919 AAGAAAAAAGAAATAGTAGCAAGTCAAGATTCAAAAT-----AAATTAGTA 966
Qy 281 ThrIleLysTyrValAspValAspThrAsnGluLeuLysSerGluGlnLeuLeuThr 300
Db 967 GATAAAGACAAATAATCTCAAAATCTAAAGATTAAAAAGAAATCTAAAGAT 1026
Qy 301 AlaSerGluArgAsnLeuAspPheArgAsp----- 310
Db 1027 TCATCAAAAAATAATTTAGACTCCAAAGATAAAGAAAAATATAAAAAAGACAAATAACATA 1086
Qy 311 -----LeuTyrAspProArgAspLysAlaLysIleLeuTyrAsnAsnLeuAspAlaPhe 328
Db 1087 AAGAAACCACTGACAAACCTTACTAAAGAAATAATTTACCAATACA----- 1134
Qy 329 GlyIleMetAsp-----TyrThrLeuThrGlyLysVal 339
Db 1135 GGATGACAGATATATTACATACGTCTAGTGTGGGTTAATT 1176

RESULT 10

US-60-615-573-7856
; Sequence 7856, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084039 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615.573
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7856

; LENGTH: 2697
; TYPE: DNA
; ORGANISM: Streptococcus agalactiae
US-60-615-573-7856
Alignment Scores:
Pred. No.: 0.0493 Length: 2697
Score: 102.00 Matches: 66
Percent Similarity: 36.53% Conservative: 52
Best Local Similarity: 20.43% Mismatches: 99
Query Match: 5.37% Indels: 106
DB: 8 Gaps: 15
US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-7856 (1-2697)
Qy 81 AspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGlyLys 100
Db 772 GATTACCATGCAATTGTA---TTTCAAGCTTTGCTGCTATTAAAGACAAGGGTGTAAAG 828
Qy 101 ValTyrPheAlaAsp-----LysAspGlySerVal 110
Db 829 ATTTATGTTACGATAAATTCGCAAGAACTTCTCGTATAGCGCTTAAGATAAACTGTT 888
Qy 111 ThrLeuProThrGlnProValGlnGluPheLeuLeuSerGlyHisValArgValArgPro 130
Db 889 AAGATTGCTGTAATTACCAAAATGATGTCAGACATATTGATAGTTTATCTGTCGCT 948
Qy 131 TyrLysGlu---LysProIleGlnAsnGlnAlaLysSerValAspValGlu----- 146
Db 949 TTGAATGAGGTTAAACCTGTTGATAATATCTTGAANAATGATGACACAGACATTAATCTC 1008
Qy 147 -----TyrThrValGlnPheThrProLeuAsnProAspAspPheArgProGly 163
Db 1009 AGCAAAACTTACCAATTAATAATACACCGACAATCTGCTCTAGAGTTT----- 1059
Qy 164 LeuLysAspThrLysLeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGlu 183
Db 1060 -----ACTATTAAATAACATTAAC 1077
Qy 184 LeuLeuAlaGlnAlaGlnSerIleLeuAsnLysAsnHisProGlyTyrThrIleTyrGlu 203
Db 1078 TCAAGTTTCAGAAATCATGACCCTTCAAGATGGAAGATGCCAGAAATGTTGTGAACAA 1137
Qy 204 ArgAspSerIleValThrHisAspAsnAspIle-----PheArgThrIleLeu--- 220
Db 1138 AAAAGATTCTTTGGATATAAACGATATGACATGATGAGTAAAGTTTAAACATTTGACTT 1197
Qy 221 ---ProMetAspGlnGluPheThrTyrArgVal----- 230
Db 1198 GGACGAAAGGATTCTGAATTTAAGGGCAACCTTATTGCAAAAACCTGGAACAGTTGAATTA 1257
Qy 231 -----LysAsnArgGluGlnAlaTyrArgIleAsnLys----- 241
Db 1258 GATATGTTTTTCAACCAATCTCAAGACCAGCTTCAATTTATTTAAAAAATAATACCTTATC 1317
Qy 242 LysSerGlyLeuAsnGluGluIleAsnAsn-----ThrAspLeu 254
Db 1318 CAAATGCTGTCCAAATGAATTTGAAAAAATTTGACTCTAGTTTGGTTTAACTGAAAGT 1377
Qy 255 IleSerGluLysTyrTyrValLeuLys----- 263
Db 1378 CAGATAGATGGATCTATATTTATAAAGATGCAATTAACCTTAAATTTAAATTAACCACT 1437
Qy 264 -----LysGlyGluLysProTyrAspProPheAspArgSer 275
Db 1438 GGTCAAGTCTTAAAGTTGTTTATAAAGGGCAAGAA---GATCCATAT-----AGT 1485
Qy 276 HisLeuLysLeuPheThrIleLysTyrValAspValAspThrAsnGluLeuLeuLysSer 295
Db 1486 CATCAGAAAGAGATATGACTAAA-----AAAGGT 1515
Qy 296 GluGlnLeuLeuThrAlaSerGluArgAsnLeuAspPheArgAspLeuTyrAspProArg 315
||||| : : : : : |||

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Db 1516 GAACAGCTCAGTCACTCACTCAACCAACCAAT-----GAA 1548
Qy 316 AspLysAlaLysLeuLeuTyrAsnAsnLeuAspAlaPheGlyIleMetAspTyrThrLeu 335
Db 1549 AATACAGCAAAAGTAACCTTTGCTAAATATTGACTGGTGCATATTAGTAAGGTACTGTG 1608
Qy 336 ThrGlyLys 338
Db 1609 AATGAAAA 1617

RESULT 11
US-10-856-118-1
; Sequence 1, Application US/10856118
; GENERAL INFORMATION:
; APPLICANT: Laidlaw, Stephen
; APPLICANT: Skinner, Mike
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Anderson, Richard
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 3742.1000-000
; CURRENT APPLICATION NUMBER: US/10/856,118
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: PCT/GB02/005411
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: GB0128733.3
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/334,649
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 266145
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fowlpox virus genome
US-10-856-118-1

Alignment Scores:
Pred. No.: 48.5 Length: 266145
Score: 101.50 Matches: 73
Percent Similarity: 34.97% Conservative: 48
Best Local Similarity: 21.10% Mismatches: 90
Query Match: 5.34% Indels: 136
DB: 6 Gaps: 17

US-09-940-235-2_COPY_16_383 (1-368) x US-10-856-118-1 (1-266145)
Qy 69 GlnGluGlnLeuIleAlaAsnValHisSerAsnAspTyrPheGluValIleAspPhe 88
Db 134861 AAAGAGAGCTGTTTCTTAAATAGATAAAATAGCTATTATTATGTTCTTGGCGGTAAG 134920
Qy 89 AlaSer---AspAlaThrIleThrAsp-----ArgAsnGlyLysValTyr 102
Db 134921 AAAATATGAGAGCTATTATTAACAGATGCTACTAGCTTCTTAAATAATACAGAATCTAT 134980
Qy 103 PheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGluPheLeuLeu 122
Db 134981 TACTGTGATCATATAGATGCG-----GAATTTATGATG 135013
Qy 123 SerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGlnAlaLysSer 142
Db 135014 TGT-----TGTAGCAAGGGAATAT----- 135034
Qy 143 ValAspValGluTyrThrValGlnPheThr-----ProLeuAsnProAspAsp 159
Db 135035 -----TATACTAATAACGGTACATGGCCTTCTATACTAAGTAGTGATCAGGAT 135082
Qy 160 PheArgProGlyLeuLysAspThrLysLeuLeuLysThrLysLeuAlaIleGlyAspThrIle 179
Db 135083 -----ACTATTGCTAGTATGCGTTGAC 135106
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Qy 180 ThrSerGlnGluLeuLeuAlaGlnSerIleLeuAsnLysAsnHisProGlyTyr 199
Db 135107 ACGCAAGAAAAAATATTATACGATCTAAAGCGTATACAAATTTATCTCCCAACAAGTAC 135166
Qy 200 ThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArgThrIle 219
Db 135167 ACATCTTATCTTACAAAATTAATAGTATTAACTAACGGTGTGATTTCTTTAGAGGACTT 135226
Qy 220 -----LeuProMetAspGlnGluPheThrTyrArgVal-----LysAsn 232
Db 135227 TACGGAATTTCTATAAATAAAGATTAATATATAGATACGAATTTATTCAGAAATTAAT 135286
Qy 233 ArgGluGlnAlaTyrArg----- 238
Db 135287 AGAGAGAATGCATTCAGAAGCATAGCTCATAAAACTATAGCTTAAATTAATTTCTAATACC 135346
Qy 239 -----IleAsnLys 241
Db 135347 GATGAAAAATATAGATGAAATTTCTACTAACATAGATGTGATTTTGTGATTTTATAAACCCAC 135406
Qy 242 LysSerGlyLeuAsnGluLeuIleAsnAsnThrAsp----- 253
Db 135407 TATACATCGTTAAATGAAGATGCTTACAAATTTGAAGATTGCCGGATATACGTGTTAAG 135466
Qy 254 -----LeuIleSerGluLysTyrTyrValLeuLysLysGlyLysPro 268
Db 135467 GATTTCTTGGAGCTTATGTCGCTAGTAAATGGTAC-----GAAGCTAAACAACAG 135517
Qy 269 TyrAspProPheAspArgSerHisLeuLysLeuPheThr-----IleLysTyrValAsp 286
Db 135518 TACGATC-TTGATCGGATATATTACAAACATTTTACAAACGTTTATAAAGTACATAGAC 135575
Qy 287 Val-----AspThrAsnGluLeuLeuLysSerGluGlnLeu----- 299
Db 135576 GTAATTATGAAAAAGAAAAAGAACGAATATATACTAAAAATGATAGAACTTTATAAATATA 135635
Qy 300 -----ThrAlaSerGluArgAsnLeu-- 306
Db 135636 GAAACATAAAATAAATACTATACTACTATTATAAACTTCTAGGAATAGAACTTCTG 135695
Qy 307 -----AspPheArgAspLeuTyrAspProArgAspLys 317
Db 135696 ATTCATATGCGTATTTGGGTATATTTGGCGCTTCAGAAATTATATAT-----AGGTTTCG 135749
Qy 317 sAlaLysLeuLeuTyr 322
Db 135750 AAGGAAGATTTCTATTT 135765

RESULT 12
US-60-615-573-12450
; Sequence 12450, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12450
; LENGTH: 945
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-12450

Alignment Scores:
Pred. No.: 0.0159 Length: 945
Score: 100.50 Matches: 48
Percent Similarity: 36.12% Conservative: 34
Best Local Similarity: 21.15% Mismatches: 70
```


Query Match: 5.23% Indels: 75
DB: 8 Gaps: 11

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-12450 (1-945)

Qy 195 AsnHisProGlyTyrThrIleTyrGluArgAspSerSerIleValThrHisAspAsnAsp 214
|||
Db 13 AATCATGCAATCATTCATCA-----AATCATTTGGAAATACAGATTAGAC 57

Qy 215 IlePhe-----ArgThrIleLeuProMet 222
|||
Db 58 AATTTTCTAAACCGGCTACTCTAATAAGCGGTGGACGACATCTGTGTGCTATCT 117

Qy 223 AspGlnGluPheThrTyrArgValLys-----AsnArgGluGlnAla 236
|||
Db 118 GATCAAAATTAAGTTTGTGCAATGACGATCGTTGGAATCTCAACCGAGACACGCT 177

Qy 237 TyrArgIleAsnLysLysSerGlyLeuAsnGluGluIleAsnAsnThrAspLeuIleSer 256
|||
Db 178 CAAGCCCTTTCTAAATTTATGAGTGTAGAGCCCAATAAGACTTTGGGATATTCTTCAA 237

Qy 257 GluLysTyrTyrValLeuLysLysGlyGluLysProTyr----- 269
|||
Db 238 ACRAAGTTTAAAGCTAAAGCACTTCAAGAAAGTTTATATTGAATATGACAAAGTGAAA 297

Qy 270 ---AspProPheAspArgSerHisLysLeuPheThrIleLysTyrValAspValAsp 288
|||
Db 298 GCAGATAGTTGGGATAGACGTAATATGCT-----ATTGAATTTAAT 339

Qy 289 ThrAsnGluLeuLysSerGluGlnLeu----- 298
|||
Db 340 CCRAACAACTTACACGAGATGAATGATTGTTGTTAAACAAATATAATAAGCTACATG 399

Qy 299 ---LeuThrAlaSerGluArgAsnLeuAspPheArg-----Asp 310
|||
Db 400 GAAGATGACGGTTTACAAAGATTAGATTGACCTTTGATTGTTGAAGATGATTGAGTGAC 459

Qy 311 LeuTyrAspProArgAspLysAla-----LysLeuLeuTyrAsnAsnLeuAspAlaPhe 328
|||
Db 460 TACTATGCAATGCTGATAAGCAGTAAAGAAACTATTTT----- 501

Qy 329 GlyIleMetAspTyrThrLeuThrGlyLysValGluAspAsnHis-----AspAsp 345
|||
Db 502 -----TATGGTCGTAATGTTAAGCCAGAACAAATATTTTGGCGTGAGAGAT 549

Qy 346 ThrAsnArgIleIleThrValTyrMetGlyLysArgProGluGlyGluAsnAla----- 363
|||
Db 550 AGTAATAGATTATTAGAAATTATAATAAAGCAAGAACGTAAGATAATATGCAGATGCT 609

Qy 364 -----SerTyrHisLeu 367
|||
Db 610 GAAGTTATGCTGAACATTTA 630

RESULT 13
US-10-956-157-943
; Sequence 943 Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 943
; LENGTH: 1584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-943

Alignment Scores:

Pred. No.: 0.039 Length: 1584
Score: 100.00 Matches: 88
Percent Similarity: 34.59% Conservative: 50
Best Local Similarity: 22.06% Mismatches: 129
Query Match: 5.26% Indels: 132
DB: 6 Gaps: 22

US-09-940-235-2_COPY_16_383 (1-368) x US-10-956-157-943 (1-1584)

Qy 27 LeuThrSerArgPro-----AlaHisGlyGly-----LysThrGluGln 39
|||
Db 25 CTGACATCCCGTGTGTTCTTCTGTGCCGGGGTCTTCTGTGCTGTGTCATGAAGACGTACCG 84

Qy 40 GlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMetSerHisLysLeu 59
|||
Db 85 GGTCTCTACAGCAGAGCCAGACTCCGGGCCCGGCGCCGCTGTGTGGCACCCTGTCG 144

Qy 60 GluLysAlaAspLeuLeuLysAlaIleGlnGluGlnLeuIleAlaAsnValHisSerAsn 79
|||
Db 145 GAGGAGCTC---TACACGAGGAAGTTGTGCATCAGCTGACA----- 183

Qy 80 AspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThrAspArgAsnGly 99
|||
Db 184 -----CTTCAGGTCTTGAATTTGTGCAGGATCCGTGC----- 216

Qy 100 LysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGlnProValGlnGlu 119
|||
Db 217 -----TTTGCCCAAGGAGATGCTCTCATTAAGCTTTATGAAAACTTTATCAGTGAA 267

Qy 120 PheLeuLeuSerGlyHisValArgValArgProTyrLysGluLysProIleGlnAsnGln 139
|||
Db 268 TTT-----GAACACAGGGTGAACCTTTGTCCCTCGTGGAATCATTTCTTCAT 315

Qy 140 AlalysSerValAspValGluTyrThrValGlnPheThrProLeuAsnProAspAsp 159
|||
Db 316 GTAGTTAGACAGATGACTGATCTTAATGTGGCTCTTACTTTCTG-----GAAAG 366

Qy 160 PheArgProGlyLeuLysAspThrLys-----LeuLeuLysThr----- 172
|||
Db 367 ACTCGTGAGAGGTGAAAGTAGTGATGAGCAGTGATCTGTGTAAACACAGCAATTGGA 426

Qy 173 -----LeuAlaIleGlyAspThrIleThrSerGlnGluLeuAlaGln 189
|||
Db 427 GCTCTAAATTTAAACATCGGGACCTACAGGTTTACAAAGAAACAATTTGAAGATGTTGAA 486

Qy 190 SerIleLeuAsnLysAsnHisProGlyTyrThr----- 200
|||
Db 487 GAAATGCTCAAC---AACCTTCTGTGTGACATCGGTTTCACAGTGTGTTCTATGATCTC 543

Qy 201 -----IleTyrGluArgAspSerSerIleValThrHisAspAsnAspIlePheArg 217
|||
Db 544 TCCAGTAATACTATCAAAACAATCGGAAACACAGCGGTCTCTACTACAAAGATGCTCTGCGG 603

Qy 218 ThrIle-----LeuProMetAspGlnGluPheThrTyrArgVal 230
|||
Db 604 TTTTGGGCTGTGTTGACATCAAGGATCTACCAGTGTCTGAGCAG----- 648

Qy 231 LysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsn----- 246
|||
Db 649 -----CAGGAGAGAGCCTTCACGCTGGGCTAGCAGGACTTCTCGGCGAGGAGTTT 702

Qy 247 -----GluGluIleAsnAsnThrAsp----- 253
|||
Db 703 AACTTTGGAGAACTCTCTCATGACCCTGTGCTGGAGTCTCCGAGGATACTGACCGGCAG 762

Qy 254 ---LeuIleSer-----GluLysTyrTyrValLeu 262
|||
Db 763 TGGCTGATTGACACCCCTCTATGCCTTCAACAGTGGCAAGTAGCGGTTCCAGACTCTG 822

Qy 263 LysLys-----GlyGluLysProTyrAspProPheAspArgSerHisLysLeuPhe 280
|||
Db 823 AAGACTGCTGGGGCCAGCAGCT----- 846

Query Match: 5.23% Indels: 93
DB: 8 Gaps: 18

US-09-940-235-2_COPY_16_383 (1-368) x US-60-615-573-7919 (1-1860)

Qy 36 LysThrGlnGlyLeuSerProLysSerLysProPheAlaThrAspSerGlyAlaMet 55
:::|||||:::|
Db 544 GAAACAGATAGAGCCTTGGAAACGTCGGATCGCGCTGTTATGTTGAAGAGCCAAACGATT 603
:::|||||:::|

Qy 56 SerHisLysLeuGluLysAlaAspLeuLeuLysAlaIleGlnGlu----- 70
|||:::|
Db 604 TCACAGCTATTACCATATTGAACAAGCTAAAGTCATTTATGAGAAAGTTTCATGGGATT 663
|||:::|

Qy 71 GlnLeuIleAlaAsn---ValHisSer----- 78
|||:::|
Db 664 CAAATTCCTCAGATGCTGTCATCAAGCAATCCGTTTATCTGTCCTATTGACACAGAT 723
|||:::|

Qy 79 -----AsnAspAspTyrPheGluValIleAspPheAlaSerAspAlaThrIleThr 95
|||:::|
Db 724 CGATTCTTGGCGGATAAGGCTTTGATTGATCGATGAAGCG-----GCGACGATTGCT 777
|||:::|

Qy 96 AspArgAsnGlyLysValTyrPheAlaAspLysAspGlySerValThrLeuProThrGln 115
|||:::|
Db 778 TCAGTTGAAGGGAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 837
|||:::|

Qy 116 -----ProValGlnGluPheLeuLeuSerGlyHisValArgValArgProTyrLys 132
|||:::|
Db 838 ACGGAATTCAGTCACTACTATCTCTAAAGGGAGATCAAGAGCGGTTAGAGGGTTTCANA 897
|||:::|

Qy 133 GluLysProIleGlnAsnGlnAlaLysSerValAsp-----ValGluTyrThrValGln 150
|||:::|
Db 898 GAAAGG---CTGATGAATCGAGTCAAAGGTCAAAGATGCCATTGAGCGCGTTGTAGAT 954
|||:::|

Qy 151 PheThrProLeuAsnProAspAspPheArgProGlyLeuLysAspThrLys----- 168
:::|
Db 955 GCGTAAACGATT-----GCTCAAGCTCGTTTACAAAATGAAAAAGGCGC 999
|||:::|

Qy 169 LeuLeuLysThrLeuAlaIleGlyAspThrIleThrSerGlnGluLeuLeuAlaGlnAla 188
|||:::|
Db 1000 CTTGCATCATCTCTTTCTCGGACCACTGGCGTGGGAAAACAGAAATAGCCAAAGCA 1059
|||:::|

Qy 189 GlnSerIleLeuAsnLysAsnHisProGlyTyrThrIleTyrGluArgAspSerSerIle 208
:::|
Db 1060 ATTGCA-----GAAGCACTTTTTTGATGATGAAGCTGCCATG 1095
|||:::|

Qy 209 ValThrHisAspAsnAspIlePheArgThrIleLeuProMetAspGlnGluPheThrTyr 228
|||:::|
Db 1096 ATTCGTTTGTATATGTCGTAGTACAAA-----CAAAAAGAAAGATGTGACTAAA 1143
|||:::|

Qy 229 ArgValLysAsnArgGluGlnAlaTyrArgIleAsnLysLysSerGlyLeuAsnGluGlu 248
|||:::|
Db 1144 CTATCGGCAATCGT-----GCCACAAGATA-----AAAGCAATTTGACTGAAGGA 1191
|||:::|

Qy 249 IleAsnAsnThrAspLeuIleSerGluLysTyrTyrValLeuLysLysGlyGluLysPro 268
|||:::|
Db 1192 GTAAAA-----CAGAAGCCT 1206
|||:::|

Qy 269 Tyr-----AspProPheAspArgSerHisLeuLysLeuPheThrIleLys 283
|||:::|
Db 1207 TATTGTCTCTGTTACTAGATGAGATTGAAAAGACACACAGTGAAGTGAAGTGAAGTGAAG 1266
|||:::|

Qy 284 TyrValAspValAspThrAsnGluLeuLysSer----- 295
|||:::|

Db 1267 TTGCAAGTGTAGATGATGTCGTTTAAACAGATAGTTCCGGTCTGTTGATTAGCTTTAAA 1326
|||:::|

Qy 296 -----GluGlnLeuLeuThrAlaSerGlu 303
|||:::|

Db 1327 AACACATTGTGATTATGACCACCAATATTGGCGCTAAAAAATCATCAATAAGTGGGAG 1386
|||:::|

Qy 304 ArgAsnLeuAspPheArgAspLeuTyrAspProArgAspLysAlaLysLeuLeuTyrAsn 323
|||:::|

Db 1387 TTGAAGGAAACCTTTAAAGATTAAACCGAT---CGAGATCGG---AAACAATTTGAAAAAG 1440
|||:::|

Qy 324 AsnLeuAspAla 327
:::|||||
Db 1441 TCGATGGACAGT 1452

Search completed: November 6, 2004, 07:42:59
Job time : 210.055 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	134.5	7.1	1985	6	US-10-732-923-3351	Sequence 3351, Ap
2	121	6.4	2400	6	US-10-732-923-22508	Sequence 22508, A
3	107	5.6	1163	6	US-10-732-923-3296	Sequence 3296, Ap
4	105	5.5	1014	6	US-10-163-587B-4	Sequence 4, Appli
5	105	5.5	1014	6	US-10-163-587B-18	Sequence 18, Appl
6	105	5.5	1014	6	US-10-163-587B-37	Sequence 37, Appl
7	105	5.5	1014	6	US-10-163-587B-38	Sequence 38, Appl
8	105	5.5	1014	6	US-10-163-587B-39	Sequence 39, Appl
9	105	5.5	1014	6	US-10-163-587B-40	Sequence 40, Appl
10	104	5.5	1445	6	US-10-732-923-8160	Sequence 8160, Ap
11	103.5	5.4	1478	6	US-10-732-923-3353	Sequence 3353, Ap
12	103	5.4	921	6	US-10-732-923-3305	Sequence 3305, Ap
13	101	5.3	509	6	US-10-732-923-22708	Sequence 22708, A
14	100.5	5.3	1430	6	US-10-797-821-36	Sequence 36, Appl
15	100	5.3	1010	6	US-10-163-587B-6	Sequence 6, Appli
16	100	5.3	1501	6	US-10-732-923-22706	Sequence 22706, A
17	100	5.3	1553	6	US-10-732-923-22705	Sequence 22705, A
18	99.5	5.2	610	6	US-10-732-923-7214	Sequence 7214, Ap
19	99.5	5.2	639	6	US-10-732-923-7215	Sequence 7215, Ap
20	99.5	5.2	1087	6	US-10-732-923-8260	Sequence 8260, Ap
21	99	5.2	1089	6	US-10-732-923-8243	Sequence 8243, Ap
22	99	5.2	1555	6	US-10-732-923-22584	Sequence 22584, A
23	99	5.2	1765	1	PCT-US04-02460-1	Sequence 1, Appli
24	98.5	5.2	2497	6	US-10-732-923-8738	Sequence 8738, Ap
25	98.5	5.2	2497	6	US-10-732-923-8739	Sequence 8739, Ap

; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES

; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 22508
; LENGTH: 2400
; TYPE: PRT
; ORGANISM: Plasmodium falciparum 3D7
US-10-732-923-22508

Query Match 6.4%; Score 121; DB 6; Length 2400;
Best Local Similarity 20.5%; Pred. No. 0.11; Mismatches 43; Indels 110; Gaps 12;
Matches 63; Conservative 43;
Qy 136 IQQAK-----SVDVEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDTITS 181
Db IKQKKIKMLNYTCPINVRYNTSYIISSSELPVGDIEIKNNMTIPCDTIILSGVTM 443
Qy 182 QELLAQAS-----ILNKHGPGYTYIERDSSIVTHDND-----IF 216
Db 444 SEHMLTGESVPIHKEQLPFEGNALINKNNKYESNDEKDDYLRYYNNHASINMIKRHLIE 503
Qy 217 RTILPMDQEF-----TY---RVKXREQAYRINKKSGLEENINNTDLI 255
Db 504 ETIGKKDREYKSNTHDLCMMNKLYINNTYDDVHMKNKMDYNNNNKKKKKINNLFV 563
Qy 256 SEKYVVLKGEKPYDPDRSHLKF-----TIKYVDVDTNELLKSEQLLTA 301
Db 564 KGTY--INSNDLLYD--DKIGVNIFEDDVNNMKHKFNQNNINYNKDTNNL----- 610
Qy 302 SERNLDRFDLYD-----PRVAKLLYNNLDAGIMDYTLTG-----KVEDN 342
Db 611 -EYNNKHRYTYDCLLKKEVAISQKNKIYSNED---INKYMLYGGTYVLSLYNINKIKYN 666
Qy 343 HDDTNRII 350
Db 667 NKEENRII 674

RESULT 3

US-10-732-923-3296
; Sequence 3296, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3296
; LENGTH: 1163
; TYPE: PRT
; ORGANISM: Clostridium acetobutylicum
US-10-732-923-3296

Query Match 5.6%; Score 107; DB 6; Length 1163;
Best Local Similarity 21.2%; Pred. No. 0.55; Mismatches 57; Indels 84; Gaps 14;
Matches 67; Conservative 57;
Qy 16 QDISLKFEDLTSRPAHGGKTEOGLSPKSPFATDSGAMSHKLEKADLLKAIQEOQLIAN 75
Db 263 KOLMEKDEIDLKEKRLGES-----SSKVKPYIDN---YENTLKQIDILK---EQIL-- 310
Qy 76 VHSNDYVEIDFASDATITDRNGKVFADKDGSTVLTPTQVQFLLSGHVVRPYKEKP 135
Db 311 --SRENTWKAISLEKE-----DMEKKLSIAKDNKEKALP-----KFMIKHHIILDAIREKD 359
Qy 136 -----IQQAQSVDEYTVQFTPLNPDDDFRGLKDTKLLKTLAIGDTITSQEL 184

Db 360 LLDNIKLEKRLQKIEKLSLEAS-----NKEELIKQNIKIDSL-TLKIQNLESKIDN 412
Qy 185 LAQAQSIILNKNHGPYTYIERDSSIVTHDNDIFRTILPMDQFTYRVKXREQAYRINKKSG 244
Db 413 LKVPPEYKKNINEG-----IFLRNDEKHKHKNKUG 444
Qy 245 LNEEINNTDL---ISEKYVVLKGEKPYDPDRSHLKLFTIKYVDVDTNELLKSEQLLTA 301
Db 445 LDCDFQVDPEKAKSKKEMLFNKLEE-----ERSKLDYTYKKLQDLN-KDPFPKDDVLLTF 498
Qy 302 SERNLDRFDLYDPRDK 317
Db 499 QEK-----LNDSRQK 508

RESULT 4

US-10-163-587B-4
; Sequence 4, Application US/10163587B
; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; TITLE OF INVENTION: AGENTS
; CURRENT APPLICATION NUMBER: US/10/163,587B
; CURRENT FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/296,110
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-587B-4

Query Match 5.5%; Score 105; DB 6; Length 1014;
Best Local Similarity 21.4%; Pred. No. 0.67;
Matches 77; Conservative 51; Mismatches 130; Indels 102; Gaps 16;
Qy 29 SRPAHGGKTEOGLSPKSPFA-----TDSGA--MSHKLEKADLLKAIQEOQLIANV 76
Db 504 SKSKGQVKKEGINKSEKRMKLTLLKGAADVDPDSGLEHSAHVLEKGGKVFSAITGLVDIV 563
Qy 77 HSNDYVEIDFASDATITDRNGKVFADK-----GSVTLPTQVQFLLSGHVVR 128
Db 564 KGTNSYKLL-----QLLEDDKENRYWIFRSGRVGTWIGSKLEQMPSEKDAIEQFMKL 617
Qy 129 RPYKEKPIQQAQSVDEYTVQFTPLNPD---DD-----FRPGLK----- 165
Db 618 --YEKGTGNASHKKNFTYKPKFYPLEIDYQDEEAVKKLTVNPGTKSLPKPVQDLIKM 675
Qy 166 --DTKLLKTLAIGDTITSQEL-----LAQAQSIILNKNHGPYTYIERDSSIVTHDND 214
Db 676 IFDVESMKAMVEYEDILQKMPGLKSKRQQAAYSILSEVQQAQVSGSSDQILDLSNR 735
Qy 215 IFRILPMDQFTYRVKXREQAYRINKKSGLEENINNTDLISEK-----YV 261
Db 736 -FYTLIPHDFGM-----KKPPL---LNNADSVQAQVEMLDNLLDIEVAYS 777
Qy 262 LKKG--EKYPDPDRSHLKLFT-IKYVDVDTNE-----LLKSEQLLTASERNLDRDLY 312
Db 778 LRGSDDSSKDPIDVNYEKLKIDIKVDVRDSEAEIIRKYVKNTHATTHSAYDLEVIDIF 837

RESULT 5

US-10-163-587B-18
; Sequence 18, Application US/10163587B
; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50229-306

RESULT 8
US-10-163-587B-39
; Sequence 39, Application US/10163587B
; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIVE AGENTS


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; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3353
; LENGTH: 1478
; TYPE: PRT
; ORGANISM: Plasmodium yoelii yoelii
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1478)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-732-923-3353

Query Match      5.4%; Score 103.5; DB 6; Length 1478;
Best Local Similarity 20.0%; Pred. No. 1.5;
Matches 76; Conservative 71; Mismatches 138; Indels 95; Gaps 19;

QY 15 NODLSLKEFFDLTSRPAHGKTE--QGLSPKSPKPFATDSGAMSHKLEKADLLKAI----- 68
DB 859 NSIINIINEIKTKNISIEKSELKKNKMLKKKYNLSNDFLQNVEDVDKLLVKE 918
QY 69 --QGLIA-----NVHS--NDYFEVIDFASDATITDRNGKYVFADKDGSVTLPTQPV 117
DB 919 SEQNELLVTENELKNLYKELNDEYNELINLIKONEYOIKNLQEOLEIKENKNT-KTBEI 977
QY 118 QEFLLS-----CHVRVRPKPKPI-----QNAKSDVDVEYT 148
DB 978 NEFLKTDLDYLTSLSQANQSLTNLSENEKNKALKQLTENIYLNQIEDKEENIYL 1037
QY 149 VOFTPLNDDDFRGLKD--TKLAKTLAIGDTITSQELLAQAQSLNKNHPGYTIYERDS 206
DB 1038 TQ--KIKSNDQVISLKEFNEMLIKKVETYSI--EELNRKEGNHTKGH-----IENS 1088
QY 207 SIVTHDNDIFRILPMDQEFYRVKNREQAYRI-----NKSGLNEEINVTDLISEKYV 261
DB 1089 TTELYDHRF-----YEDIDKNELGVISKLENDNNLNKEE--CDMLKNDFYI 1134
QY 262 LKGEKPYDPDRSHLKLFTIKYVD--VD-TNELLKSEOLLTASER-----NL 306
DB 1135 L--SEKHLEEEITQKNDLPKYNDDELIDKNDIIEKENLINERNKYIKIKQIIDICFNK 1192
QY 307 DFRDLYDPRDKALLYNNLD 326
DB 1193 DF-SIIDIREKIVAIFENDD 1211

RESULT 12
US-10-732-923-3305
; Sequence 3305, Application US/10732923.
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 3305
; LENGTH: 921
; TYPE: PRT
; ORGANISM: Fusobacterium nucleatum subsp. vincentii ATCC 49256
US-10-732-923-3305

Query Match      5.4%; Score 103; DB 6; Length 921;
Best Local Similarity 18.7%; Pred. No. 0.86;
Matches 84; Conservative 74; Mismatches 123; Indels 168; Gaps 20;

QY 36 KTEOGLSPKSPKPFATD-----SGAMSHKLEKAD--LLKAIQEQ-----LIANVH 77
DB 460 KSKSELNKKICPFLNEKQCNLEDEADYFSSKISIKTLEDLENLKNIEBKQILVEKV 519
QY 78 SND----DYFEVIDFASDATITDRNGKYVFADKDGSVTLPTQPV-----QEFLLSGHVR 128
DB 520 PEDRKQYFELEKSIKDLSELKNEEINLKEIHELDKNLDMMNKKLIENQEFQNSQMLR- 578
QY 129 RPYKEKPIQNAQSVDEVYVQFTPLNPDDEFPRGLKDTKLKTLAIGDTITSQELLAQA 188
DB 579 --EKKELEVELRNLM-----DEKRNKLN--LLENLE-----TEKELIKN 617
QY 189 QSLNKN-----HFGYTIYERDSSIVTHDN-----DI 215
DB 618 QNSIESNLKKIDIEFSSKIKVDTNKNIESIKSEIKTFENKLDLKNPVEYLNKNNVLAEDL 677
QY 216 FRTILPMDQEFYRVKNREQAYRI-----NKSGLNEEINN--TDLISEKYVVLKKG 265
DB 678 ENLLKVD-----KNIKELYSRLTRDKNLLKKEKVSILBEKIKNIDELKEKYDIKE- 729
QY 266 EKPYDPDRSHLKLFTIKYVDVDTNELLS-----BOLLTASERN---L 306
DB 730 -----ELNEINKKLGSSQEKIENYKYLEKISSQEEKEKKLLI 767
QY 307 DFRDLYDPRDKALLYNNLDLAFG--IMDYTLTG-----KVEDNHDDTN 347
DB 768 EFKLENKFNKANLIRNEVGQMGRAISKYMLSGISNIAVNFNKITGRITERIENWSEED 827
QY 348 RIITYVMGRPE-----GENASYHLA 368
DB 828 KYAVYLVGQERKIAPEQLSGGQSVVAIA 856

RESULT 13
US-10-732-923-22708
; Sequence 22708, Application US/10732923
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52796)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO 22708
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-732-923-22708

Query Match      5.3%; Score 101; DB 6; Length 509;
Best Local Similarity 19.2%; Pred. No. 0.56;
Matches 69; Conservative 59; Mismatches 115; Indels 116; Gaps 17;

QY 37 TEOGLSPKSPKPFATDSGAMSHKLEKADLLKATQELIA---NVHSNDYDFEVIDFASDAT 93
DB 179 SHONINGNNKQYSSSSGLIISNAPK----REISSRVISFKSKKKNYIFNAPVPTS--S 232
QY 94 ITRDRNGKV--YFADKDGSVTLPTQPVQEFLLSG-----HVRVRPYKEKPIQNAQSV 143
DB 233 LIEELGQIEYIFSDKTGTLTCNIMEFRKCAINGISYKGLTEIKRNILKKNLE-----I 287
QY 144 DVEYTVQFTPLNP-----DDDFRPGDKD-----TKLAKTLAIGDTITSQELLAQAQ 189
DB 288 PVEPTMKFKKTPHVNIIIDNDIINHLKDPNHNHVNLIINFFLHLAINHAV----- 337
QY 190 SILKNHPGYTIYERDS-----SIVT-----HNDIFRILPMDQ-----E 225
DB 338 -ICEKDKEGVTYSSSSPDEALVNAAKHFDITFLYRREGKYGISIFGKIYEIDTLATIE 396
QY 226 FTYRVKNREQAYRI-----NKSGLNEEINNTDLISEKYVVLKKGKPK----- 268
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Db 397 FTSKRMSVICRIPVINPDYHPTDAKSNMCKQNMDD---DHLVVGKNEKEETDD 452
Qy 269 ---YDPDRSHLKLFTIKYVDVDNELLKSQLTASERNLDFRDLYDPRDKAKLLYN 324
Db 453 LNVTPPKKEAHKUL-----NNN-----NNNRIDNLDYDKKNFNIIYH 492

RESULT 14
US-10-797-821-36
; Sequence 36, Application US/10797821
; GENERAL INFORMATION:
; APPLICANT: Smith, Daniel J.
; APPLICANT: Taubman, Martin A.
; TITLE OF INVENTION: Glucan Binding Protein and Glycosyltransferase Immunogens
; FILE REFERENCE: 25669-020
; CURRENT APPLICATION NUMBER: US/10/797,821
; PRIOR FILING DATE: 2004-03-09
; PRIOR APPLICATION NUMBER: 10/383,930
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: 60/363,209
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/402,483
; PRIOR FILING DATE: 2002-08-08
; PRIOR APPLICATION NUMBER: 09/290,049
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 60/081,550
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/115,142
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 36
; LENGTH: 1430
; TYPE: PRT
; ORGANISM: Streptococcus mutans
US-10-797-821-36

Query Match 5.3%; Score 100.5; DB 6; Length 1430;
Best Local Similarity 20.5%; Pred. No. 2.5;
Matches 102; Conservative 77; Mismatches 163; Indels 155; Gaps 26;

Qy 6 SVAGTVESTNQDISLKFEID--LTSRPAHGKTEQGLSPKSPKFPATDSGAMSHKLEKAD 63
Db 91 STSITKETPSQNIITQANSDDKTNTKSEEAQSEERTKQSEEAQTITASSQALTAQAE 150
Qy 64 LLKAIQEOLIANVHNSDDYFVIDPASDATITDRNGKVFADKGSVTLTPQVQEFLLS 123
Db 151 LTK--QRQTAQENKNP-----VDLAAIPNVKQIDGKYIYIGSDG-----QPKKNFALT 197
Qy 124 GHVRVPYKEK-----PIQNOAKSVDEVYTVQFTPLN----- 155
Db 198 VNNKLVFDKNTGALTDTSTQFQKGLTKLNDYTPHNOIVNFPNTSLETIDNYYVTADSW 257
Qy 156 ---PDD-----DPRPGL-----KDTKLL-----KTLAIGDITIT---SQE 183
Db 258 YRPKDLKNGKTWTASSESDLRPLMSWPKQTQIAVLNVMNQOGLGTGENYTADSSQE 317
Qy 184 ---LLAQ-----QSILN---KNHPGYTIY-EROSIVTHNDIERT 218
Db 318 SLNLAAQTQVVKIETKISQTQOTQWLRIINSFVKTPQNMNSQTESDTSAGEKDHLOGGA 377
Qy 219 ILPMDQBEFT-----YRVKNR-----EQAYRINKKSG-----LNBEINNTDLISEK-- 258
Db 378 LLYSNSOKTAYANSYRLNLTPTSTQTKPKYFEDNSSGGYDFLLANDIDNSNPVVAEQ 437
Qy 259 ----YYVLKKG-----EKPYDPDRSHLKLFTIKVVDV-----TNELKSEQLLTASERN- 305
Db 438 LNWHLNMYGSIIVANDEANFD--GVRVDAVDNVDNADLLQIASDYLKAHYGVKSEKNA 495
Qy 306 ---LDPRDLYDPRDK-----AKLYNNLDFAFGIMDYTLTGKVEDNHDNTRI----- 349
Db 496 INHLSILEAWSDNDPQVKNKTKGAQLPIDNKLRLSL--YALTRPLEKDAKNKEIRSGLE 554
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Qy 350 ---ITVYMGR-PEGENA 363
Db 555 PVIITNSLNRSAGKNS 571

RESULT 15
US-10-163-587B-6
; Sequence 6, Application US/10163587B
; GENERAL INFORMATION:
; APPLICANT: OLIVEIRA, MARCOS
; TITLE OF INVENTION: SELECTIVE PARP-1 TARGETING FOR DESIGNING CHEMO/RADIO SENSITIZING
; FILE REFERENCE: 50229-306
; CURRENT APPLICATION NUMBER: US/10/163,587B
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/296,110
; PRIOR FILING DATE: 2001-06-07
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 6
; LENGTH: 1010
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-163-587B-6

Query Match 5.3%; Score 100; DB 6; Length 1010;
Best Local Similarity 20.8%; Pred. No. 1.7;
Matches 75; Conservative 54; Mismatches 129; Indels 102; Gaps 16;

Qy 29 SRPAHGKTEQGLSPKSPFA-----TDSGA--MSHKLEKADLLKAIQEOLIANV 76
Db 500 SKKSGAVKEGKVNKSEKRMKLTLLKGGAAVDPDGLGSAHVLEKGGKVFSAATLGLVDIV 559
Qy 77 HSNDDYFEVIDPASDATITDRNGKVFADK-----GSVTLTPQVQEFLLSGHVRV 128
Db 560 KGTNSYYKL-----QLLEDDKESRYWIFRSWGRVGTIGSNKLSQMPSEKDAVEHFMKL 613
Qy 129 RPYKEPIQNOAKSVDEVYTVQFTPLNPD---DD-----PRPGLK----- 165
Db 614 --YEKTNANHSHKSNFTKYPKFPLEIDYGOEEAVKKLTVKPGTKSKLKPQVQELVGM 671
Qy 166 --DTKLLKTLAIGDITITSQEL-----LAQASILNKNHPGYTIYERDSIVTHDND 214
Db 672 IFDVESMKALVEVEIDLQKMPGLKLSRRQIAQAYSILSEVQOAVSQSSSQILDLSNR 731
Qy 215 IFRILPMDQBEFTYRVKREQAYRINKKSGLINEEINNTDLISEK-----YYV 261
Db 732 -FYTLIPHDFGM-----KKPPL---LNNADSVQAKVEMLDNLLDIEVAYSIL 773
Qy 262 LKKG--EKPYDPDRSHLKLFT-IKVVDVDTNE-----LLKSEQLLTASERNLDFRDLY 312
Db 774 LRGSDDSSKQPIDVNYEKLKTDIKVDRDSEAEVIRKYVKNTHATTNAYDLEVIDIF 833

Search completed: November 4, 2004, 00:11:48
Job time : 15.863 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:38:12 ; Search time 34.0925 Seconds
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Title: US-09-940-235-4_COPY_150_259

Perfect score: 627

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Searched: 693957 seqs, 115811272 residues

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Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV.TIMEOUT=120 -WARN TIMEOUT=130 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: /cgn2_6/ptodata/2/pna/US07_NEW_COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	627	100.0	2127	6	US-10-956-157-4288
2	627	100.0	2402	1	PCT-US04-31524-364
3	627	100.0	7677	6	US-10-956-157-4995
4	627	100.0	7680	6	US-10-948-737-4446
5	627	100.0	7912	1	PCT-US04-31524-366
6	627	100.0	8272	1	PCT-US04-31524-370
7	627	100.0	8374	1	PCT-US04-31524-374
8	627	100.0	8449	1	PCT-US04-31524-190
9	627	100.0	8647	1	PCT-US04-31524-368
10	627	100.0	8815	1	PCT-US04-31524-372

11	627	100.0	8815	6	US-10-868-577A-62	Sequence 62, Appl	
12	218	34.8	600	6	US-10-956-160-215929	Sequence 215929, Ap	
13	218	34.8	1567	6	US-10-956-160-5822	Sequence 5822, Ap	
14	213	34.0	600	6	US-10-956-157-9521	Sequence 9521, Ap	
15	213	34.0	607	6	US-10-948-737-12304	Sequence 12304, A	
16	213	34.0	1400	6	US-10-956-157-10230	Sequence 10230, A	
17	213	34.0	2384	6	US-10-956-157-4286	Sequence 4286, Ap	
18	201	32.1	600	6	US-10-956-157-9523	Sequence 9523, Ap	
19	165	26.3	588	6	US-10-956-157-4994	Sequence 4994, A	
20	165	26.3	588	6	US-10-956-157-10229	Sequence 10229, A	
21	165	26.3	1241	6	US-10-956-157-234	Sequence 234, App	
22	165	26.3	1241	6	US-10-956-157-5469	Sequence 5469, Ap	
23	119.5	19.1	600	6	US-10-956-160-215928	Sequence 215928, Ap	
24	119.5	19.1	794	6	US-10-956-160-5821	Sequence 5821, Ap	
c	25	89	14.2	7017	6	US-10-956-157-413	Sequence 413, App
26	81	12.9	407	6	US-10-964-549-799	Sequence 799, App	
27	76.5	12.2	609	6	US-10-948-737-3916	Sequence 3916, Ap	
c	28	74	11.8	565	6	US-10-948-737-7910	Sequence 7910, Ap
c	29	73	11.6	327	6	US-10-948-737-4102	Sequence 4102, Ap
c	30	73	11.6	328	6	US-10-948-737-4224	Sequence 4224, Ap
c	31	73	11.6	385	6	US-10-948-737-4808	Sequence 4808, Ap
c	32	73	11.6	421	6	US-10-948-737-775	Sequence 775, App
c	33	73	11.6	446	6	US-10-948-737-1057	Sequence 1057, App
c	34	73	11.6	448	6	US-10-220-366A-13515	Sequence 13515, A
c	35	73	11.6	499	6	US-10-948-737-1099	Sequence 1099, Ap
c	36	72	11.5	420	6	US-10-220-366A-13860	Sequence 13860, A
c	37	72	11.5	1186	8	US-60-613-292-977	Sequence 977, App
c	38	72	11.5	4743	6	US-10-956-157-4104	Sequence 4104, Ap
c	39	71.5	11.4	2808	6	US-10-956-157-1543	Sequence 1543, Ap
c	40	71.5	11.4	6761	6	US-10-960-275-1	Sequence 1, Appl
c	41	71.5	11.4	7561	6	US-10-967-702-21	Sequence 21, Appl
c	42	71	11.3	1082	6	US-10-486-706-211	Sequence 211, App
c	43	71	11.3	1400	6	US-10-956-157-6117	Sequence 6117, Ap
c	44	71	11.3	2914	6	US-10-956-157-882	Sequence 882, App
c	45	70.5	11.2	660	8	US-60-615-573-18478	Sequence 18478, A

ALIGNMENTS

RESULT 1
US-10-956-157-4288
; Sequence 4286, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4288
; LENGTH: 2127
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4288

Alignment Scores:
Pred. No.: 1.96e-63 Length: 2127
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-157-4288 (1-2127)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 597 CCCATAGCTGAGAGTGTGTTTTCATGCTGCTGGACTTCCTATGCTGCGGAGAAACG 656
Qy 21 TrpGluLysProTyrGlnGlyTrpMetValAspCysThrCysLeuGlyGluGlySer 40

Db 657 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTCTCTGGGAGAAGGCG 716
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 717 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 776
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 777 AGAATTGGAGACACTGGAGCAAGAGGATTAATCGAGGAACCTGCTCCAGTGATCTGC 836
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 837 ACAGCAACGCCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGACAGCACCATCG 896
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 897 AGCGGATCTGGCCCTTCACCGATGTTCTGT 926

RESULT 2

PCT-US04-31524-364
; Sequence 364, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 364
; LENGTH: 2402
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-364

Alignment Scores:
Pred. No.: 2,31e-63 Length: 2402
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_copy_150_259 (1-110) x PCT-US04-31524-364 (1-2402)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 807 CCCATAGCTGAGAAGTGTGTTGATCATGCTCTGGACTTCTCTATGTTGGTCGGAAGACG 866
Qy 21 TrpGluLysProTyrGlnGlyTrpMetValAspCysThrCysLeuGlyGlySer 40
Db 867 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTCTCTGGACTTCTCTATGTTGGTCGGAAGACG 926
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 986
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 987 AGAATTGGAGACACTGGAGCAAGAGGATAATCGAGGAACCTGCTCCAGTGATCTGC 1046
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 1047 ACAGCAACGCCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGACAGCACCATCG 1106
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1107 AGCGGATCTGGCCCTTCACCGATGTTCTGT 1136

RESULT 3

US-10-956-157-4995
; Sequence 4995, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4995
; LENGTH: 7677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4995

Alignment Scores:

Pred. No.: 1,06e-62 Length: 7677
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-157-4995 (1-7677)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 461 CCCATAGCTGAGAAGTGTGTTGATCATGCTCTGGACTTCTCTATGTTGGTCGGAAGACG 520
Qy 21 TrpGluLysProTyrGlnGlyTrpMetValAspCysThrCysLeuGlyGlySer 40
Db 521 TGGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTCTCTGGACTTCTCTATGTTGGTCGGAAGACG 580
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 581 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT 640
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysileCys 80
Db 641 AGAATTGGAGACACTGGAGCAAGAGGATAATCGAGGAACCTGCTCCAGTGATCTGC 700
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 701 ACAGCAACGCCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGACAGCACCATCG 760
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 761 AGCGGATCTGGCCCTTCACCGATGTTCTGT 790

RESULT 4

US-10-948-737-4446
; Sequence 4446, Application US/10948737
; GENERAL INFORMATION:
; APPLICANT: CHAN, VIVIEN W.
; APPLICANT: ESCOBEDO, JAIME
; APPLICANT: GARCIA, PABLO DOMINGUEZ
; APPLICANT: HANSEN, RHONDA
; APPLICANT: KAUFMANN, JOERG
; APPLICANT: KENNEDY, GIULIA C.
; APPLICANT: LAMSON, GEORGE
; APPLICANT: MOLER, EDWARD J.
; APPLICANT: RANDAZZO, FILIPPO
; APPLICANT: REINHARD, CHRISTOPH
; APPLICANT: SUDDUTH-KUINGER, JULIE
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED
; FILE REFERENCE: 2300-21987
; CURRENT APPLICATION NUMBER: US/10/948,737


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; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 8647
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-368

Alignment Scores:
Pred. No.: 1.24e-62 Length: 8647
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x PCT-US04-31524-368 (1-8647)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 807 CCCATAGCTGAGAAGTGTGTTTATCATGCTCTGGGACTTCTTATGTTGGTGGAGAAACG 866

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 867 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGTATTGTTACTTGGCTGGAGAAGGACG 926

Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 986

Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 987 AGAATTGGAGACACCTGGAGCAAGAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 1046

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrSer 100
Db 1047 ACAGGCAACGCCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGAGACCATCG 1106

Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1107 AGCGGATCTGCCCTTCACCGATGTTTGT 1136

RESULT 10
; Sequence 62, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alicalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-577A-62

Alignment Scores:
Pred. No.: 1.28e-62 Length: 8815
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-868-577A-62 (1-8815)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 807 CCCATAGCTGAGAAGTGTGTTTATCATGCTCTGGGACTTCTTATGTTGGTGGAGAAACG 866

Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 867 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGTATTGTTACTTGGCTGGAGAAGGACG 926

Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 927 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 986

Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 987 AGAATTGGAGACACCTGGAGCAAGAGGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 1046

Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrSer 100
Db 1047 ACAGGCAACGCCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGAGACCATCG 1106

Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1107 AGCGGATCTGCCCTTCACCGATGTTTGT 1136

PCT-US04-31524-372
; Sequence 372, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-372

Alignment Scores:
Pred. No.: 1.28e-62 Length: 8815
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
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Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 1107 AGCGAATCTGGCCCTTCACCGATGTTCTGT 1136

RESULT 12
US-10-956-160-215929
; Sequence 5822, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215929
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-215929
Alignment Scores:
Pred. No.: 1,44e-16 Length: 600
Score: 218.00 Matches: 35
Percent Similarity: 55.91% Conservatives: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 34.77% Indels: 2
Gaps: 6
DB: 1

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-160-215929 (1-600)
; Sequence 5822, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215929
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-215929
Alignment Scores:
Pred. No.: 1,44e-16 Length: 600
Score: 218.00 Matches: 35
Percent Similarity: 55.91% Conservatives: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 34.77% Indels: 2
Gaps: 6
DB: 1

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-160-215929 (1-600)
Qy 1 ProtlealaGluLysCysPheAspHisAlaAlaGlyThrSerTyrrValValGlyGluThr 20
Db 273 CCTACAGATGACTCGTCTGCACCCCTACACGGTTTCCCATTTATGCTTGGAGAGGAG 332
Qy 21 TrpGluLysProTyrrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 333 TGGAGCGGTGTCTGAATCTGGCTTTAAGCTCTCGGCCAGTCTTAGGCTTTGGCAGT 392
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyrr 60
Db 393 GGTCAATTCAGATGTGACTCATCTAAATGGTGCCATGATAATGGT-----GTGAACACTAC 446
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysileCys 80
Db 447 AAGATTGGCAGAGATGCGATCGTCAGGGGAGAGATGCGCCAGATGATGATGATGATGATGAT 506
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHis 93
Db 507 CTGGAATGAAAGAGAGATTCAGTGTGATCTTCAT 545

RESULT 13
US-10-956-160-5822
; Sequence 5822, Application US/10956160
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES
; FILE REFERENCE: 031896-044000 (AM101084)
; CURRENT APPLICATION NUMBER: US/10/956.160
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 222274
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5822
; LENGTH: 1567
; TYPE: DNA
; ORGANISM: Canis familiaris
US-10-956-160-5822
Alignment Scores:
Pred. No.: 5,09e-16 Length: 1567
Score: 218.00 Matches: 35
Percent Similarity: 55.91% Conservatives: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 34.77% Indels: 2
Gaps: 6
DB: 1

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-160-5822 (1-1567)
Qy 1 ProtlealaGluLysCysPheAspHisAlaAlaGlyThrSerTyrrValValGlyGluThr 20
Db 1240 CCTACAGATGACTCGTCTGCACCCCTACACGGTTTCCCATTTATGCTTGGAGAGGAG 1299
Qy 21 TrpGluLysProTyrrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 1300 TGGAGCGGTGTCTGAATCTGGCTTTAAGCTCTCGGCCAGTCTTAGGCTTTGGCAGT 1359
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyrr 60
Db 1360 GGTCAATTCAGATGTGACTCATCTAAATGGTGCCATGATAATGGT-----GTGAACACTAC 1413
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysileCys 80
Db 1414 AAGATTGGCAGAGATGCGATCGTCAGGGGAGAGATGCGCCAGATGATGATGATGATGATGAT 1473
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHis 93
Db 1474 CTGGAATGAAAGAGAGATTCAGTGTGATCTTCAT 1512

RESULT 14
US-10-956-157-9521
; Sequence 9521, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9521
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9521
Alignment Scores:
Pred. No.: 5,5e-16 Length: 600
Score: 213.00 Matches: 35
Percent Similarity: 55.91% Conservatives: 17
Best Local Similarity: 37.63% Mismatches: 39
Query Match: 33.97% Indels: 2
Gaps: 6
DB: 1

US-09-940-235-4_COPY_150_259 (1-110) x US-10-956-157-9521 (1-600)
Qy 1 ProtlealaGluLysCysPheAspHisAlaAlaGlyThrSerTyrrValValGlyGluThr 20
Db 40 CCTACGGATGACTCGTCTGTGACCCCTACACAGTTTCCCATTTATGCGTGGAGATGAG 99
Qy 21 TrpGluLysProTyrrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
Db 100 TGGGAACGACATGCTCTGAATCAGGCTTTAAACTGTTGTCAGTCTTAGGCTTTGGAAGT 159
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GenCore version 5.1.6
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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	100.0	777	21	US-09-471-349-3
2	600	100.0	777	40	US-09-940-235-3
3	600	100.0	777	57	US-10-631-558-3
4	600	100.0	1661	21	US-09-471-349-10
5	600	100.0	1661	40	US-09-940-235-10
6	600	100.0	1661	57	US-10-631-558-10
7	600	100.0	6988	49	US-10-236-392-1
8	600	100.0	7341	1	PCT-US01-14827-4096
9	600	100.0	7341	25	US-09-577-408-5027
10	600	100.0	7679	48	US-10-155-653-38
11	600	100.0	7679	62	US-10-831-704-38
12	600	100.0	7680	2	PCT-US02-02176-1216
13	600	100.0	7680	2	PCT-US02-10824-60
14	600	100.0	7680	2	PCT-US02-14877A-654
15	600	100.0	7680	2	PCT-US02-15982-75
16	600	100.0	7680	2	PCT-US02-15982A-75
17	600	100.0	7680	2	PCT-US02-18638A-63
18	600	100.0	7680	2	PCT-US04-07268-79
19	600	100.0	7680	2	PCT-US04-15421-122
20	600	100.0	7680	15	US-09-053-375B-1319
21	600	100.0	7680	21	US-09-440-302A-1117
22	600	100.0	7680	21	US-09-440-302B-1117
23	600	100.0	7680	21	US-09-442-589B-1143
24	600	100.0	7680	24	US-09-543-679A-2698
25	600	100.0	7680	43	US-09-964-824C-574
26	600	100.0	7680	43	US-09-964-824C-574
27	600	100.0	7680	48	US-10-171-311-63
28	600	100.0	7680	48	US-10-182-936A-75
29	600	100.0	7680	49	US-10-219-051B-9261
30	600	100.0	7680	49	US-10-236-031B-69
31	600	100.0	7680	49	US-10-240-851-75
32	600	100.0	7680	50	US-10-278-698-88
33	600	100.0	7680	50	US-10-278-698-603
34	600	100.0	7680	52	US-10-374-979-75
35	600	100.0	7680	54	US-10-470-050-1216
36	600	100.0	7680	54	US-10-477-173-654
37	600	100.0	7680	54	US-10-477-238A-654
38	600	100.0	7680	57	US-10-641-643-1289

39 600 100.0 7680 57 US-10-680-287A-654
 40 600 100.0 7680 60 US-10-717-597-222
 41 600 100.0 7680 61 US-10-788-792-79
 42 600 100.0 7680 62 US-10-843-641A-5877
 43 600 100.0 7680 95 US-60-230-071-75
 44 600 100.0 7680 108 US-60-427-982-222
 45 600 100.0 7680 111 US-60-459-782-222

ALIGNMENTS

RESULT 1
 US-09-471-349-3
 ; GENERAL INFORMATION:
 ; SEQUENCE 3, Application US/09471349
 ; APPLICANT: Sahni, Girish
 ; APPLICANT: Kumar, Rajesh
 ; APPLICANT: Roy, Chaiti
 ; APPLICANT: Rajagopal, Kammara
 ; APPLICANT: Nihalani, Deepak
 ; APPLICANT: Sundaram, Vasudha
 ; APPLICANT: Yadav, Mahavir
 ; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
 ; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
 ; FILE REFERENCE: 07064/009001
 ; CURRENT APPLICATION NUMBER: US/09/471,349
 ; CURRENT FILING DATE: 1999-12-23
 ; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
 ; PRIOR FILING DATE: 1998-12-24
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 777
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)....(777)
 US-09-471-349-3

Alignment Scores:
 Pred. No.: 1.09e-59 Length: 777
 Score: 600.00 Matches: 106
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-09-471-349-3 (1-777)

QY 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
 DB 1 CAGGCTCAGCAATGGTTTCAGCCCGGTCGCGTCCAGTCAAGCAAGCCCGGT 60
 QY 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnTnTnGluArgThrTyrLeuGly 40
 DB 61 TGTATGCAATGAAACACATATCAGATAATCAACAGTGGGACGCGACCTACCTAGGT 120
 QY 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
 DB 121 AATGTTGGTTTGTACTTGTATGGAGAGCCGAGGTTTAACTCGGAAGTAAACCT 180
 QY 61 GluAlaGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
 DB 181 GAAGCTGAAGAGACTTGTCTTTCACAAAGTACACTTACGAGTGGGTGACACT 240
 QY 81 TyrGluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
 DB 241 TATGAGCGTCTCAAGACTCCATGATCTGGGACTGATCTGATCGGGGCTGGGAGGG 300
 QY 101 ArgIleSerCysThrIle 106

; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
; FILE REFERENCE: 07064/009001
; CURRENT APPLICATION NUMBER: US/09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated primer
US-09-471-349-10

Alignment Scores:
Pred. No.: 2,78e-59 Length: 1661
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-09-940-235-4_COPY_1_106 (1-106) x US-09-471-349-10 (1-1661)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1341 CAGCGCAGCAAAATGGTTTCAGCCCCAGTCCCGGTGGTGTCAAGCAAGCCCGGT 1400
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 1401 TGTATGACAAATGGAACACATATCAGATAATCAACAGTGGAGCGGACCTACCTAGGT 1460
Qy 41 AsnValLeuValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 1461 AATGTGTGGTTTGTACTTGTATGGAGAAAGCGAGGTTTTAACTGCGAAAGTAAACCT 1520
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 1521 GAAGCTGAAGAGACTTGTCTTTGACAAGTACACTGGAACTTACCGAGTGGTGACACT 1580
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 1581 TATGAGCGTCTTAAGACTCCATGATCTGGAGCTGTACTGCATCGGGCTGGCGAGGG 1640
Qy 101 ArgIleSerCysThrIle 106
Db 1641 AGAATAAGCTGTACCATC 1658

RESULT 5
US-09-940-235-10
; Sequence 10, Application US/09940235
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/09/940,235
; CURRENT FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-09-940-235-10
Alignment Scores:
Pred. No.: 2,78e-59 Length: 1661
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0
US-09-940-235-4_COPY_1_106 (1-106) x US-09-940-235-10 (1-1661)
Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1341 CAGCGCAGCAAAATGGTTTCAGCCCCAGTCCCGGTGGTGTCAAGCAAGCCCGGT 1400
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 1401 TGTATGACAAATGGAACACATATCAGATAATCAACAGTGGAGCGGACCTACCTAGGT 1460
Qy 41 AsnValLeuValCysThrCysTyrGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 1461 AATGTGTGGTTTGTACTTGTATGGAGAAAGCGAGGTTTTAACTGCGAAAGTAAACCT 1520
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 1521 GAAGCTGAAGAGACTTGTCTTTGACAAGTACACTGGAACTTACCGAGTGGTGACACT 1580
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 1581 TATGAGCGTCTTAAGACTCCATGATCTGGAGCTGTACTGCATCGGGCTGGCGAGGG 1640
Qy 101 ArgIleSerCysThrIle 106
Db 1641 AGAATAAGCTGTACCATC 1658
RESULT 6
US-10-631-558-10
; Sequence 10, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahn, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammara
; APPLICANT: Nihalani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 1661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid cassette
US-10-631-558-10

Alignment Scores:
Pred. No.: 2.78e-59 Length: 1661
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-631-558-10 (1-1661)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 1341 CAGGCGCAGCAAAATGTTTCAGCCCACTCCCGGTGGTGTCTCAGTCAAGCAAGCCCGGT 1400

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnIntrpGluArgThrTyrLeuGly 40
Db 1401 TGTATGACATGGAATAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 1460

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 1461 AATGTGTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTTAACTGCGAAGTAAACCT 1520

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 1521 GAAGCTGAAGAGACTTCTTTGACCAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 1580

Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 1581 TATGAGCGTCTCTAAAGACTCCATCATCTGGGACTGTACCTGCATCGGGCTGGGCGAGGG 1640

Qy 101 ArgIleSerCysThrIle 106
Db 1641 AGAATAAGCTGTACCATC 1658

RESULT 7
US-10-236-392-1
; Sequence 1, Application US/10236392
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Caeman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
```

```
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennnda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 1
; LENGTH: 6988
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26)...(6986)
US-10-236-392-1

Alignment Scores:
Pred. No.: 1.63e-58 Length: 6988
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 49 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-236-392-1 (1-6988)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGTTTCAGCCCACTCCCGGTGGTGTCTCAGTCAAGCAAGCCCGGT 73

Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnIntrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACATGGAATAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133

Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTGTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTTAACTGCGAAGTAAACCT 193

Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTTGACAAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 253

Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTCTAAAGACTCCATCATCTGGGACTGTACCTGCATCGGGCTGGGCGAGGG 313

Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331
```

```
RESULT 8
PCT-US01-14827-4096
; Sequence 4096, Application PC/TUS0114827
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-104
; CURRENT APPLICATION NUMBER: PCT/US01/14827
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/577,408
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 16102
; SOFTWARE: Custom
; SEQ ID NO 4096
; LENGTH: 7341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(7338)
; OTHER INFORMATION: 100% homologous to Homo sapiens Fibrinogen-alpha, accession
; OTHER INFORMATION: number AAR60021, Smith-Waterman Score=13183.
PCT-US01-14827-4096

Alignment Scores:
Pred. No.: 1,74e-58 Length: 7341
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US01-14827-4096 (1-7341)
Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 94 CAGGCTCAGCAAAATGGTTTCAGCCCGAGTCCCGGTGGTGTGTCAGTCAAGCAAGCCCGGT 153
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 154 TGTATGACAAATGGAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 213
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 214 AATGTTGGTTTGTACTTGTATGAGGAGGAGCGAGGTTTAACTGCGAAGTAAACCT 273
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 274 GAAGCTGAAGAGACTTGTCTTTCAGCAAGTACACTTGGGAACACTTACCGAGTGGGTGACACT 333
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 334 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGCATCGGGCTGGCGGAGGG 393
Qy 101 ArgIleSerCysThrIle 106
Db 394 AGAATAAGCTGTACCATC 411

RESULT 9
US-09-577-408-5027
; Sequence 5027, Application US/09577408
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Tillinghast, John
; APPLICANT: Sinku, Ankura
; APPLICANT: Liu, Chenghua
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 792
; CURRENT APPLICATION NUMBER: US/09/577,408
; CURRENT FILING DATE: 2000-05-18
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; NUMBER OF SEQ ID NOS: 8502
; SOFTWARE: pt_gct_genes Version 1.0
; SEQ ID NO 5027
; LENGTH: 7341
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (82)..(7338)
; OTHER INFORMATION: similar to gi31397 in the genepept database release 115,
; OTHER INFORMATION: Run with FASTXY 3.3t00, default parameters
US-09-577-408-5027

Alignment Scores:
Pred. No.: 1,74e-58 Length: 7341
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 25 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-09-577-408-5027 (1-7341)
Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 94 CAGGCTCAGCAAAATGGTTTCAGCCCGAGTCCCGGTGGTGTGTCAGTCAAGCAAGCCCGGT 153
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 154 TGTATGACAAATGGAACACATATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 213
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 214 AATGTTGGTTTGTACTTGTATGAGGAGGAGCGAGGTTTAACTGCGAAGTAAACCT 273
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 274 GAAGCTGAAGAGACTTGTCTTTCAGCAAGTACACTTGGGAACACTTACCGAGTGGGTGACACT 333
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 334 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGCATCGGGCTGGCGGAGGG 393
Qy 101 ArgIleSerCysThrIle 106
Db 394 AGAATAAGCTGTACCATC 411

RESULT 10
US-10-155-653-38
; Sequence 38, Application US/10155653
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE IDENTIFICATION AND
; TITLE OF INVENTION: ASSESSMENT
; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 07334-074001
; CURRENT APPLICATION NUMBER: US/10/155,653
; CURRENT FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: US/09/220,132
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: US 60/079,303
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: US 60/068,821
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 7679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-155-653-38

Alignment Scores:
```

Qy	21	CysTyrAspAenGlyLysHisTyrGlnIleAenGlnIntrpGluArgThrTyrLeuGly	40
Db	74	TGTTATGACAAATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGT	133
Qy	41	AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60
Db	134	AATGTGTTGGTTGTGACTTGTATTGAGAGAAAGCCGAGGTTTAACTGCGAAAGTAAACCT	193
Qy	61	GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr	80
Db	194	GAAGCTGAAGAGACTTGCTTTTGACAAGTACACTGGGAACACTTACCGAGTGGGTGACACT	253
Qy	81	TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly	100
Db	254	TATGAGCGTCTAAAGACTCCATGATCTGGGACTGTACTGTCATCGGGGCTGGCGAGGG	313
Qy	101	ArgIleSerCysThrIle	106
Db	314	AGAATAAGCTGTACCATC	331

RESULT 12

PCT-US02-02176-1216

; Sequence 1216, Application PC/TUS0202176

; GENERAL INFORMATION:

; APPLICANT: Orr, Michael S.

; APPLICANT: Nation, Michele

; APPLICANT: Diggans, James C.

; APPLICANT: Zeng, Wen

; APPLICANT: Gene Logic, Inc.

; TITLE OF INVENTION: Gene Expression Profiles in Breast Tissue

; FILE REFERENCE: 44921-5070-WO

; CURRENT APPLICATION NUMBER: PCT/US02/02176

; CURRENT FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: US 60/263,757

; PRIOR FILING DATE: 2001-01-25

; PRIOR APPLICATION NUMBER: US 60/286,090

; PRIOR FILING DATE: 2001-04-25

; PRIOR APPLICATION NUMBER: US 60/292,517

; PRIOR FILING DATE: 2001-05-23

; NUMBER OF SEQ ID NOS: 1246

; SOFTWARE: PatentIn ver. 2.1

; SEQ ID NO 1216

; LENGTH: 7680

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURES:

; OTHER INFORMATION: Genbank Accession No. X02761

PCT-US02-02176-1216

Alignment Scores:

Pred. No.:	1.84e-58	Length:	7680
Score:	600.00	Matches:	106
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-940-235-4_COPY 1_106 (1-106) x PCT-US02-02176-1216 (1-7680)

Qy	1	GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly	20
Db	14	CAGGCTCAGCAAAATGGTTTACGCCAGTCCCGGTGGCTGTTCAGTCAAAGCAAGCCCGGT	73
Qy	21	CysTyrAspAenGlyLysHisTyrGlnIleAenGlnIntrpGluArgThrTyrLeuGly	40
Db	74	TGTTATGACAAATGGAACACATATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGT	133
Qy	41	AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60
Db	134	AATGTGTTGGTTGTGACTTGTATTGAGAGAAAGCCGAGGTTTAACTGCGAAAGTAAACCT	193
Qy	61	GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr	80

Db 194 GAAGCTGAAGAGACTTGTCTTGACAAAGTACACTGGGAACACTTACCAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGCGGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331
RESULT 13
PCT-US02-10824-60
; Sequence 60, Application PC/TUS0210824
; GENERAL INFORMATION:
; APPLICANT: Origene Technologies
; TITLE OF INVENTION: Prostate Cancer Expression Profiles
; FILE REFERENCE: 9U 206 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10824
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/281,732
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/281,731
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-10824-60

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_copy_1_106 (1-106) x PCT-US02-10824-60 (1-7680)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGCTCAGCAATGGTTTCAGCCCGTCCCGGTGGTGTCAAGCAAGCCCGGT 73
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACAATGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTGTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTAACTCGAAAGTAAACCT 193
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTGACAAAGTACACTGGGAACACTTACCAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGCGGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

RESULT 14
PCT-US02-14877A-654
; Sequence 654, Application PC/TUS0214877A
; GENERAL INFORMATION:
; APPLICANT: Genome Therapeutics Corporation and
; APPLICANT: Allen, Kristina M.
; APPLICANT: Yaworsky, Paul

; APPLICANT: Morales, Arturo J.
; APPLICANT: Graham, James R.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: HBM Variants that Modulate Bone Mass and Lipid Levels
; FILE REFERENCE: 032796-135
; CURRENT APPLICATION NUMBER: PCT/US02/14877A
; CURRENT FILING DATE: 2002-05-13
; PRIOR APPLICATION NUMBER: US 60/290,071
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/291,311
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 1086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 654
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14877A-654

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US02-14877A-654 (1-7680)

Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGCTCAGCAATGGTTTCAGCCCGTCCCGGTGGTGTCAAGCAAGCCCGGT 73
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATGACAATGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACCTAGGT 133
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTGTGGTTTGTACTTGTATGGAGGAAGCCGAGGTTTAACTCGAAAGTAAACCT 193
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTGACAAAGTACACTGGGAACACTTACCAGTGGGTGACACT 253
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGCGGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

RESULT 15
PCT-US02-15982-75
; Sequence 75, Application PC/TUS0215982
; GENERAL INFORMATION:
; APPLICANT: Allen, Kristina M.
; APPLICANT: Anisowicz, Anthony
; APPLICANT: Bhat, Bheem
; APPLICANT: Damagnez, Veronique
; APPLICANT: Robinson, John
; APPLICANT: Yaworsky, Paul
; TITLE OF INVENTION: Reagents and Method for Modulating DKK-Mediated Interactions
; FILE REFERENCE: 032796-132
; CURRENT APPLICATION NUMBER: PCT/US02/15982
; CURRENT FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/291,311

; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/353,058
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: US 60/361,293
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 214
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 7680
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-15982-75

Alignment Scores:
Pred. No.: 1.84e-58 Length: 7680
Score: 600.00 Matches: 106
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US02-15982-75 (1-7680)

QY 1_GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTTCAGCCCGGCTCCCGGGTGTCTCAGTCAAAGCAAGCCCGGT 73
QY 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThrTyrLeuGly 40
Db 74 TGTATTGACAAATGGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTTACCTAGGT 133
QY 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATGTTTGGTTTGTACTTGTATGGAGAGAGCCGAGGTTTAACTGCGAAAGTAAACT 193
QY 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTGTCTTTGACAAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 253
QY 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTCTAAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGGCTGGGCGAGGG 313
QY 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

Search completed: November 6, 2004, 07:38:44
Job time: 1744.21 secs

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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:38:12 ; Search time 32.8527 Seconds
(without alignments)
747.335 Million cell updates/sec

Title: US-09-940-235-4_COPY_1_106

Perfect score: 600

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delopt 6.0 , Delopt 7.0

Searched: 63957 seqs, 115811272 residues

Total number of hits satisfying chosen parameters: 1387914

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=Pending Patents NA New -QFMT=fastap -SUFFIX=p2n.rnnp -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cgi -LIST=45 -DOLALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
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-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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4: /cgn2_6/ptodata/2/pna/US08 NEW COMB.seq.*
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6: /cgn2_6/ptodata/2/pna/US10 NEW COMB.seq.*
7: /cgn2_6/ptodata/2/pna/US11 NEW COMB.seq.*
8: /cgn2_6/ptodata/2/pna/US60 NEW COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	100.0	7680	6	US-10-948-737-4446 Sequence 4446, Ap
2	596	99.3	2127	6	US-10-956-157-4288 Sequence 4288, Ap
3	596	99.3	2402	1	PCT-US04-31524-364 Sequence 364, App
4	596	99.3	7677	6	US-10-956-157-4995 Sequence 4995, Ap
5	596	99.3	7912	1	PCT-US04-31524-366 Sequence 366, App
6	596	99.3	8272	1	PCT-US04-31524-370 Sequence 370, App
7	596	99.3	8374	1	PCT-US04-31524-374 Sequence 374, App
8	596	99.3	8449	1	PCT-US04-31524-190 Sequence 190, App
9	596	99.3	8647	1	PCT-US04-31524-368 Sequence 368, App
10	596	99.3	8815	1	PCT-US04-31524-372 Sequence 372, App

11	596	99.3	8815	6	US-10-868-577A-62 Sequence 62, Appl
12	317	52.8	407	6	US-10-964-549-799 Sequence 799, App
13	162.5	27.1	588	6	US-10-956-157-4994 Sequence 4994, App
14	162.5	27.1	588	6	US-10-956-157-10229 Sequence 10229, A
15	162.5	27.1	600	6	US-10-956-157-9521 Sequence 9521, Ap
16	162.5	27.1	1241	6	US-10-956-157-234 Sequence 234, App
17	162.5	27.1	1241	6	US-10-956-157-5469 Sequence 5469, Ap
18	162.5	27.1	1400	6	US-10-956-157-10230 Sequence 10230, A
19	162.5	27.1	2384	6	US-10-956-157-4286 Sequence 4286, Ap
20	147.5	24.6	607	6	US-10-948-737-12304 Sequence 12304, A
21	138.5	23.1	600	6	US-10-956-160-215929 Sequence 215929,
22	138.5	23.1	1567	6	US-10-956-160-5822 Sequence 5822, Ap
23	135	22.5	600	6	US-10-956-157-9523 Sequence 9523, Ap
24	130.5	21.8	600	6	US-10-956-160-215928 Sequence 215928,
25	130.5	21.8	794	6	US-10-956-160-5821 Sequence 5821, Ap
26	116.5	19.4	609	6	US-10-948-737-3916 Sequence 3916, Ap
27	93	15.5	13715	6	US-10-399-103A-365 Sequence 365, App
28	91	15.2	268	6	US-10-220-366A-7529 Sequence 7529, Ap
29	87	14.5	502	6	US-10-954-094-130 Sequence 130, App
30	87	14.5	775	6	US-10-954-094-116 Sequence 116, App
31	87	14.5	1032	6	US-10-954-094-98 Sequence 98, Appl
32	87	14.5	1305	6	US-10-954-094-84 Sequence 84, Appl
33	75	12.5	2853	6	US-10-961-020-3 Sequence 3, Appl1
34	75	12.5	3446	6	US-10-961-020-7 Sequence 7, Appl1
35	74	12.3	3650	6	US-10-956-157-5017 Sequence 5017, Ap
36	74	12.3	3665	6	US-10-956-157-2573 Sequence 2573, Ap
37	73	12.2	2036	6	US-10-956-157-642 Sequence 642, App
38	72.5	12.1	3201	6	US-10-650-650-17 Sequence 17, Appl
39	72.5	12.1	3657	6	US-10-650-650-2 Sequence 2, Appl1
C 40	72	12.0	4469	8	US-60-613-292-875 Sequence 875, App
41	71.5	11.9	2958	6	US-10-956-157-1891 Sequence 1891, Ap
C 42	70.5	11.8	2061	6	US-10-956-373-15 Sequence 15, Appl
C 43	70.5	11.8	2437	6	US-10-956-373-13 Sequence 13, Appl
C 44	70.5	11.7	4647	6	US-10-956-373-9 Sequence 9, Appl1
45	70	11.7	1395	6	US-10-662-425-11 Sequence 11, Appl

ALIGNMENTS

RESULT 1

US-10-948-737-4446

; Sequence 4446, Application US/10948737

; GENERAL INFORMATION:

; APPLICANT: CHAN, VIVIEN W.

; APPLICANT: ESCOBEDO, JAIME

; APPLICANT: GARCIA, PABLO DOMINGUEZ

; APPLICANT: HANSEN, RHONDA

; APPLICANT: KAUFMANN, JOERG

; APPLICANT: KENNEDY, GIULIA C.

; APPLICANT: LAMSON, GEORGE

; APPLICANT: MOLIER, EDWARD J.

; APPLICANT: RANDAZZO, FILIPPO

; APPLICANT: REINHARD, CHRISTOPH

; APPLICANT: SUDDUTH-KLINGER, JULIE

; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED

; TITLE OF INVENTION: IN CANCEROUS CELLS III

; FILE REFERENCE: 2300-21987

; CURRENT FILING DATE: 2004-09-22

; PRIOR APPLICATION NUMBER: 10/616,900

; PRIOR FILING DATE: 2003-07-09

; PRIOR APPLICATION NUMBER: 09/872,850

; PRIOR FILING DATE: 2001-06-01

; PRIOR APPLICATION NUMBER: 60/208,871

; PRIOR FILING DATE: 2000-06-02

; PRIOR APPLICATION NUMBER: 10/081,519

; PRIOR FILING DATE: 2002-02-21

; PRIOR APPLICATION NUMBER: 60/270,959

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 10/310,673

; PRIOR FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/336,613

; PRIOR FILING DATE: 2001-12-04


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Db 540 GAAGCTGAAGAGACTTGGTTTGAACGATACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrgluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 4
US-10-956-157-4995
; Sequence 4995, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE REFERENCE: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4995
; LENGTH: 7677
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4995

Alignment Scores:
Pred. No.: 9,98e-67 Length: 7677
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-956-157-4995 (1-7677)
Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 14 CAGGCTCAGCAAAATGGTTTCAGCCCGAGTCCCGGTGGCTGTCTAGTCAAGCAAGCCCGGT 73
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnThrGluArgThrTyrLeuGly 40
Db 74 TGTATGACAAATGGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACTAGGC 133
Qy 41 AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 134 AATCGGTGGTTGTACTTGTATGGAGGAGCCGAGGTTTAACTCGAGAGTAAACCT 193
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 194 GAAGCTGAAGAGACTTCTTTCAGCAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 253
Qy 81 TyrgluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
Db 254 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGGCGAGGG 313
Qy 101 ArgIleSerCysThrIle 106
Db 314 AGAATAAGCTGTACCATC 331

RESULT 5
PCT-US04-31524-366
; Sequence 366, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01

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; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 366
; LENGTH: 7912
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-366

Alignment Scores:
Pred. No.: 1.04e-66 Length: 7912
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-366 (1-7912)
Qy 1 GlnAlaGlnGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAAAATGGTTTCAGCCCGAGTCCCGGTGGCTGTCTAGTCAAGCAAGCCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnThrGluArgThrTyrLeuGly 40
Db 420 TGTATGACAAATGGAAACACTATCAGATAAATCAACAGTGGGAGCGGACCTACTAGGC 479
Qy 41 AsnValIleuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro 60
Db 480 AATCGGTGGTTGTACTTGTATGGAGGAGCCGAGGTTTAACTCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 540 GAAGCTGAAGAGACTTCTTTCAGCAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrgluArgProLysAspSerMetIleThrAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAGACTCCATGATCTGGGACTGTACCTGTCATCGGGCTGGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 6
PCT-US04-31524-370
; Sequence 370, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 370
; LENGTH: 8272
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-370

Alignment Scores:
Pred. No.: 1.1e-66 Length: 8272
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0

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DB:	1	Gaps:	0
US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-370 (1-8272)			
Qy	1	GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly	20
Db	360	CAGGCTCAGCAAAATGGTTCAGCCCGAGTCCCGGTGGCTGTCAAGTCAAGCAAGCCCGGT	419
Qy	21	CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTyrGluArgThrTyrLeuGly	40
Db	420	TGTTATGACAATGGAAACAACACTATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGC	479
Qy	41	AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60
Db	480	AATCGGTTGGTTTGTTACTTGTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCT	539
Qy	61	GluAlaGluGlnThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr	80
Db	540	GAGAGCTGAAGAGACTTGCTTTGACAAGTACACTGGGAACACTTCCGAGTGGGTGACACT	599
Qy	81	TyrGluArgProLysAspSerMetIleTyrPaspCysThrCysIleGlyAlaGlyArgGly	100
Db	600	TATGAGCGTCTTAAAGACTCATGATCTGGGACTGTACTGCATCGGGCTGGCGGAGG	659
Qy	101	ArgIleSerCysThrIle 106	
Db	660	AGAATAGCTGTACCATC 677	
RESULT 7			
PCT-US04-31524-374			
; Sequence 374, Application PC/TUS0431524			
; GENERAL INFORMATION:			
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.			
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS			
; FILE REFERENCE: DFN-054PC			
; CURRENT APPLICATION NUMBER: PCT/US04/31524			
; CURRENT FILING DATE: 2004-10-01			
; PRIOR APPLICATION NUMBER: 60/506221			
; PRIOR FILING DATE: 2003-09-25			
; PRIOR APPLICATION NUMBER: 60/509594			
; PRIOR FILING DATE: 2003-10-08			
; NUMBER OF SEQ ID NOS: 381			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 374			
; LENGTH: 8374			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
PCT-US04-31524-374			
Alignment Scores:			
Pred. No.:	1,12e-66	Length:	8374
Score:	596.00	Matches:	105
Percent Similarity:	99.06%	Conservative:	0
Best Local Similarity:	99.06%	Mismatches:	1
Query Match:	99.33%	Indels:	0
DB:	1	Gaps:	0
US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-374 (1-8374)			
Qy	1	GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly	20
Db	360	CAGGCTCAGCAAAATGGTTCAGCCCGAGTCCCGGTGGCTGTCAAGTCAAGCAAGCCCGGT	419
Qy	21	CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTyrGluArgThrTyrLeuGly	40
Db	420	TGTTATGACAATGGAAACAACACTATCAGATAAATCAACAGTGGAGCGGACCTACCTAGGC	479
Qy	41	AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnCysGluSerLysPro	60
Db	480	AATCGGTTGGTTTGTTACTTGTATGGAGGAAGCCGAGGTTTTAACTGCGAGAGTAAACCT	539
Qy	61	GluAlaGluGlnThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr	80

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; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 368
; LENGTH: 8647
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-368

Alignment Scores:
Pred. No.: 1.17e-66 Length: 8647
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-368 (1-8647)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAAGAACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 480 AATGGTTGGTTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 540 GAAGCTGAAGAGACTTGTCTTTCAGCAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGCTGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 10
PCT-US04-31524-372
; Sequence 372, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 372
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US04-31524-372

Alignment Scores:
Pred. No.: 1.2e-66 Length: 8815
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-372 (1-8815)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAAGAACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 480 AATGGTTGGTTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 660 AGAATAAGCTGTACCATC 677
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Query Match: 99.33% Indels: 0
DB: 1 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x PCT-US04-31524-372 (1-8815)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAAGAACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 480 AATGGTTGGTTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
Db 540 GAAGCTGAAGAGACTTGTCTTTCAGCAAGTACACTGGGAACACTTACCGAGTGGGTGACACT 599
Qy 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100
Db 600 TATGAGCGTCTTAAAGACTCCATGATCTGGGACTGTACCTGCATCGGGCTGGCGAGGG 659
Qy 101 ArgIleSerCysThrIle 106
Db 660 AGAATAAGCTGTACCATC 677

RESULT 11
US-10-868-577A-62
; Sequence 62, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alicata et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 62
; LENGTH: 8815
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-868-577A-62

Alignment Scores:
Pred. No.: 1.2e-66 Length: 8815
Score: 596.00 Matches: 105
Percent Similarity: 99.06% Conservative: 0
Best Local Similarity: 99.06% Mismatches: 1
Query Match: 99.33% Indels: 0
DB: 6 Gaps: 0

US-09-940-235-4_COPY_1_106 (1-106) x US-10-868-577A-62 (1-8815)

Qy 1 GlnAlaGlnMetValGlnProGlnSerProValAlaValSerGlnSerLysProGly 20
Db 360 CAGGCTCAGCAATGGTTTCAGCCCCAGTCCCGGCTGTCAGTCAAGCAAGCCCGGT 419
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnInTrpGluArgThrTyrLeuGly 40
Db 420 TGTATGACATGGAAGAACATATCAGATAAATCAACAGTGGAGCGGACCTTACCTAGGC 479
Qy 41 AsnValLeuValCysThrCysTyrGlyGlySerArgGlyPheAsnGlySerLysPro 60
Db 480 AATGGTTGGTTTGTACTTGTATGGAGGAGCCGAGGTTTAACTGCGAGAGTAAACCT 539
Qy 61 GluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGlyAspThr 80
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Db 540 GAACTGAAGAGACTTGGTTTTGACAAGTACACTGGGAACACTTTACCGAGTGGGTGCACT 599

QY 81 TyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGlyArgGly 100

Db 600 TATGAGCGCTCTTAAGACTCCATCATCTGGGACTGTACTCGGGCTGGGCGAGGG 659

QY 101 ArgIleSerCysThrIle 106

Db 660 AGAATAAGCTGTACCATC 677

RESULT 12

```

US-10-964-549-799
; Sequence 799, Application US/10964549
; GENERAL INFORMATION:
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and Animals
; FILE REFERENCES: LEX-0286-USA
; CURRENT APPLICATION NUMBER: US/10/964,549
; CURRENT FILING DATE: 2004-10-13
; PRIOR APPLICATION NUMBER: US/09/750,456
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 09/728,445
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/168,358
; PRIOR FILING DATE: 1999-12-01
; NUMBER OF SEQ ID NOS: 891
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 799
; LENGTH: 407
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(407)
; OTHER INFORMATION: n = A,T,C or G
US-10-964-549-799

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4994
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4994

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; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4994
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-4994

Alignment Scores:
Pred. No.: 4.82e-12 Length: 588
Score: 162.50 Matches: 32
Percent Similarity: 57.32% Conservatives: 15
Best Local Similarity: 39.02% Mismatches: 28
Query Match: 27.08% Indels: 7
DB: 6 Gaps: 4

US-09-940-235-4_COPY_1_106 (1-106) x US-10-956-157-4994 (1-588)
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThr
Db 70 TGCATGACATGTGTGTGACTACAGACTTCGAGAGAGAGTGGGACCGTCA
Qy 40 GlyAsnValLeuValCysThrCysTyrGlyGlySerArgGly---PheAsAs
Db 130 GCCAGATGATGAGTCACATGCTTGGGAACGGAAAAGGAGAAATTCAA
Qy 59 LysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTy
Db 190 CAT-----GAGGCAACGCTGTTATGAT-----GATGGGAAGACATA
Qy 79 AspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysLil
Db 235 GAACAGTGGCAGAGGAATATCTCGGTGCCATTGTCTCTGCACATGCTT
Qy 99 ArgGly 100
Db 295 CGGGGC 300

RESULT 14
US-10-956-157-10229
; SEQUENCE INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXP
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10229
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10229

Alignment Scores:
Pred. No.: 4.82e-12 Length: 588
Score: 162.50 Matches: 32
Percent Similarity: 57.32% Conservatives: 15
Best Local Similarity: 39.02% Mismatches: 28
Query Match: 27.08% Indels: 7
DB: 6 Gaps: 4

US-09-940-235-4_COPY_1_106 (1-106) x US-10-956-157-10229 (1-588)
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnGlnTrpGluArgThr

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Db 70 TGCCATGACAAATGGTGTGAACACTACAAGATTGGAGAGAAAGTCGGACCCGTCAGGGAGAAAAT 129
Qy 40 GlyAsnValLeuValCysThrCysTyrGlyGlySerArgGly---PheAsnCysGluSer 58
Db 130 GGCAGATGATGAGCTGCACATGCTCTGGGAACGGAAAAGAGAAATTCAGTGTGACCCCT 189
Qy 59 LysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGly 78
Db 190 CAT-----GAGGCAACGTGTATGAT-----GATGGGAAGACATACCACGTAGGA 234
Qy 79 AspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGly 98
Db 235 GAACAGTGGCAGAGAAGAAATATCTCGTGCCATTGCTCTGCACATGCTTTGGAGGCCAG 294
Qy 99 ArgGly 100
Db 295 CGGGGC 300

RESULT 15
US-10-956-157-9521
; Sequence 9521, Application US/10956157
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; FILE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9521
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-9521

Alignment Scores:
Pred. No.: 4.95e-12 Length: 600
Score: 162.50 Matches: 32
Percent Similarity: 57.32% Conservative: 15
Best Local Similarity: 39.02% Mismatches: 28
Query Match: 27.08% Indels: 7
DB: 6 Gaps: 4

US-09-940-235-4_COPY_1_106 (1-106) x US-10-956-157-9521 (1-600)
Qy 21 CysTyrAspAsnGlyLysHisTyrGlnIleAsnGlnTrpGluArgThr---TyrLeu 39
Db 190 TGCCATGACAAATGGTGTGAACACTACAAGATTGGAGAGAAAGTCGGACCCGTCAGGGAGAAAAT 249
Qy 40 GlyAsnValLeuValCysThrCysTyrGlyGlySerArgGly---PheAsnCysGluSer 58
Db 250 GGCAGATGATGAGCTGCACATGCTCTGGGAACGGAAAAGAGAAATTCAGTGTGACCCCT 309
Qy 59 LysProGluAlaGluGluThrCysPheAspLysTyrThrGlyAsnThrTyrArgValGly 78
Db 310 CAT-----GAGGCAACGTGTATGAT-----GATGGGAAGACATACCACGTAGGA 354
Qy 79 AspThrTyrGluArgProLysAspSerMetIleTrpAspCysThrCysIleGlyAlaGly 98
Db 355 GAACAGTGGCAGAGAAGAAATATCTCGTGCCATTGCTCTGCACATGCTTTGGAGGCCAG 414
Qy 99 ArgGly 100
Db 415 CGGGGC 420
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Search completed: November 6, 2004, 07:43:07
Job time : 40.8527 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 00:21:37 ; Search time 1800.68 Seconds
(without alignments)
2477.164 Million cell updates/sec

Title: US-09-940-235-4_COPY150_259

Perfect score: 627

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Ygapop 10.0 ,	Ygapext 0.5
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Delop 6.0 ,	Delext 7.0

Searched: 44308572 seqs, 20275418765 residues

Total number of hits satisfying chosen parameters: 88617144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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56:	/cgn2_6/ptodata/1/pna/US105B_COMB.seq:
57:	/cgn2_6/ptodata/1/pna/US106A_COMB.seq:
58:	/cgn2_6/ptodata/1/pna/US107A_COMB.seq:
59:	/cgn2_6/ptodata/1/pna/US107B_COMB.seq:
60:	/cgn2_6/ptodata/1/pna/US107C_COMB.seq:
61:	/cgn2_6/ptodata/1/pna/US107D_COMB.seq:
62:	/cgn2_6/ptodata/1/pna/US108A_COMB.seq:
63:	/cgn2_6/ptodata/1/pna/US108B_COMB.seq:
64:	/cgn2_6/ptodata/1/pna/US109A_COMB.seq:
65:	/cgn2_6/ptodata/1/pna/US6000_COMB.seq:
66:	/cgn2_6/ptodata/1/pna/US6001_COMB.seq:
67:	/cgn2_6/ptodata/1/pna/US6002_COMB.seq:
68:	/cgn2_6/ptodata/1/pna/US6003_COMB.seq:
69:	/cgn2_6/ptodata/1/pna/US6004_COMB.seq:
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72:	/cgn2_6/ptodata/1/pna/US6007_COMB.seq:
73:	/cgn2_6/ptodata/1/pna/US6008_COMB.seq:
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75:	/cgn2_6/ptodata/1/pna/US6010_COMB.seq:
76:	/cgn2_6/ptodata/1/pna/US6011_COMB.seq:
77:	/cgn2_6/ptodata/1/pna/US6012_COMB.seq:
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86:	/cgn2_6/ptodata/1/pna/US6021_COMB.seq:
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93:	/cgn2_6/ptodata/1/pna/US6027_COMB.seq:
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96:	/cgn2_6/ptodata/1/pna/US6030_COMB.seq:
97:	/cgn2_6/ptodata/1/pna/US6031_COMB.seq:
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 104: /cgn2_6/ptodata/1/pna/US6038_COMB.seq:
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 106: /cgn2_6/ptodata/1/pna/US6040_COMB.seq:
 107: /cgn2_6/ptodata/1/pna/US6041_COMB.seq:
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 109: /cgn2_6/ptodata/1/pna/US6043_COMB.seq:
 110: /cgn2_6/ptodata/1/pna/US6044_COMB.seq:
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 114: /cgn2_6/ptodata/1/pna/US6048_COMB.seq:
 115: /cgn2_6/ptodata/1/pna/US6049_COMB.seq:
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 117: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:
 118: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:
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 120: /cgn2_6/ptodata/1/pna/US6054_COMB.seq:
 121: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:
 122: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:
 123: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:
 124: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:
 125: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	627	100.0	357	21	Sequence 6693, Ap
2	627	100.0	357	21	Sequence 6818, Ap
3	627	100.0	777	21	Sequence 3, Appli
4	627	100.0	777	21	Sequence 3, Appli
5	627	100.0	777	57	Sequence 3, Appli
6	627	100.0	1446	28	Sequence 762, App
7	627	100.0	1446	28	Sequence 9663, Ap
8	627	100.0	1446	30	Sequence 10150, A
9	627	100.0	1541	21	Sequence 9, Appli
10	627	100.0	1541	40	Sequence 9, Appli
11	627	100.0	1541	57	Sequence 9, Appli
12	627	100.0	1926	25	Sequence 41, Appl
13	627	100.0	1926	25	Sequence 41, Appl
14	627	100.0	2096	21	Sequence 12, Appl
15	627	100.0	2096	40	Sequence 12, Appl
16	627	100.0	2096	57	Sequence 12, Appl
17	627	100.0	2127	2	Sequence 49, Appl
18	627	100.0	2127	49	Sequence 49, Appl
19	627	100.0	2127	116	Sequence 4288, Ap
20	627	100.0	2147	25	Sequence 2, Appli
21	627	100.0	2147	25	Sequence 2, Appli
22	627	100.0	2147	25	Sequence 2, Appli
23	627	100.0	2402	64	Sequence 1138, Ap
24	627	100.0	2402	123	Sequence 1138, Ap
25	627	100.0	2443	2	Sequence 1483, Ap
26	627	100.0	2443	2	Sequence 70, Appl
27	627	100.0	2443	61	Sequence 238, App
28	627	100.0	2443	61	Sequence 70, Appl
29	627	100.0	2443	61	Sequence 111, App
30	627	100.0	2443	64	Sequence 1127, Ap
31	627	100.0	2443	122	Sequence 61, Appl
32	627	100.0	2443	123	Sequence 1474, Ap
33	627	100.0	2488	2	Sequence 75, Appl
34	627	100.0	2488	2	Sequence 244, App
35	627	100.0	2488	61	Sequence 244, App
36	627	100.0	2488	61	Sequence 75, Appl
37	627	100.0	2488	61	Sequence 117, App
38	627	100.0	2488	64	Sequence 1141, Ap

ALIGNMENTS

RESULT 1

US-09-431-517-6693
 ; Sequence 6693, Application US/09431517
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-751CON1
 ; CURRENT APPLICATION NUMBER: US/09/431,517
 ; CURRENT FILING DATE: 1999-11-01
 ; EARLIER APPLICATION NUMBER: US 09/170,294
 ; EARLIER FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 31760
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 6693
 ; LENGTH: 357
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-431-517-6693

Alignment Scores:

Pred. No.: 1.56e-55 Length: 357
 Score: 627.00% Matches: 110
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-431-517-6693 (1-357)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
 Db 7 CCCATAGCTGAGAAGTGTTCATCATCTGCTGGACTTCCTATGCTGGAGAAACG 66
 Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer 40
 Db 67 TGGGAGAAGCCCTACCAAGGCTGGATGATGGTAGATTGTACTTGCCTGGGAGAGCAGC 126
 Qy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
 Db 127 GGAGCGATCATCTGCACCTTCTAGAAATAGATCAACAGATCAGACACAAAGGACATCTAT 186
 Qy 61 ArgIleGlyAspThrTrpSerIlysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
 Db 187 AGAATTGGAGACACCTGGAGCAAGAGGTAATCGAGGAAACCTGCTCCAGTGCATCTGC 246
 Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
 Db 247 ACAGCAACGCCCGAGGAGAGTGGAAAGTGTGAGAGGCACACCTCTGTGAGACCAACATCG 306
 Qy 101 SerGlySerGlyProPheThrAspValArg 110
 Db 307 AGCGATCTGCCCTTCACCGATGTTCTGT 336

RESULT 2

US-09-431-517-6818
 ; Sequence 6818, Application US/09431517
 ; GENERAL INFORMATION:
 ; APPLICANT: Hyseq, Inc
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
 ; FILE REFERENCE: 20411-751CON1

Sequence 67, Appl
 Sequence 1487, Ap
 Sequence 1167, Ap
 Sequence 984, App
 Sequence 984, App
 Sequence 212, App
 Sequence 269, App

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; CURRENT APPLICATION NUMBER: US 09/431,517
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: US 09/170,294
; EARLIER FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 31760
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6818
; LENGTH: 357
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-431-517-6818

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Alignment Scores:
Pred. No.:      1.56e-55      Length:      357
Score:          627.00      Matches:     110
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      MisMatches:  0
Query Match:    100.00%      Indels:      0
DB:             21          Gaps:        0

US-09-940-235-4  COPY 150 259 (1-110) x US-09-431-517-6818 (1-357)

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-940-235-3 (1-777)

```
Oy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 448 CCCATAGCTGAGAAGTGTGTTGATCATGCTGGACTTCCTATGTTGGTGGAGAAACG 507

Oy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGluGlySer 40
Db 508 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAAGCAGC 567

Oy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 568 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 627

Oy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 628 AGAATTGGAGACACCTGGAGCAAGAGGATAATCGAGGAACCTGCTCCAGTGCATCTGC 687

Oy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 688 ACAGCAACGCCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACACATCG 747

Oy 101 SerGlySerGlyProPheThrAspValArg 110
Db 748 AGCGGATCTGGCCCTTCACCGATGTTGGT 777
```

RESULT 5

US-10-631-558-3
; Sequence 3, Application US/10631558
; GENERAL INFORMATION:
; APPLICANT: Kumar, Rajesh
; APPLICANT: Sahni, Girish
; APPLICANT: Roy, Chait
; APPLICANT: Rajagopal, Kammar
; APPLICANT: Nihalani, Deepak
; APPLICANT: Yadav, Mahavir
; APPLICANT: Sundaram, Vasudha
; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE
; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION
; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID
; TITLE OF INVENTION: PROTEIN
; FILE REFERENCE: 07064-009002
; CURRENT APPLICATION NUMBER: US/10/631,558
; CURRENT FILING DATE: 2003-07-31
; PRIOR APPLICATION NUMBER: US/09/940,235
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 09/471,349
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: IN 3825/DEL/98
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(777)
US-10-631-558-3

Alignment Scores:
Pred. No.: 3,87e-55 Length: 777
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 57 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-10-631-558-3 (1-777)

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Oy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 448 CCCATAGCTGAGAAGTGTGTTGATCATGCTGGACTTCCTATGTTGGTGGAGAAACG 507

Oy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGluGlySer 40
Db 508 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAAGCAGC 567

Oy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 568 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 627

Oy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 628 AGAATTGGAGACACCTGGAGCAAGAGGATAATCGAGGAACCTGCTCCAGTGCATCTGC 687

Oy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 688 ACAGCAACGCCCGAGGAGAGTGGAAGTGTGAGAGGCACACCTCTGTGCAGACACATCG 747

Oy 101 SerGlySerGlyProPheThrAspValArg 110
Db 748 AGCGGATCTGGCCCTTCACCGATGTTGGT 777
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RESULT 6

US-09-641-529-762
; Sequence 762, Application US/09641529
; GENERAL INFORMATION:
; APPLICANT: Gearing, David P.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 1600.1156-001
; CURRENT APPLICATION NUMBER: US/09/641,529
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,798
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 1042
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 762
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-641-529-762

Alignment Scores:
Pred. No.: 8e-55 Length: 1446
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 28 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-641-529-762 (1-1446)

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Oy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 814 CCCATAGCTGAGAAGTGTGTTGATCATGCTGGACTTCCTATGTTGGTGGAGAAACG 873

Oy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGluGlySer 40
Db 874 TGGGAGAAGCCCTACCAAGGCTGGATGATGTTAGATTGTTACTTGCCTGGGAGAAGCAGC 933

Oy 41 GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 934 GGACGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACAAAGGACATCCTAT 993

Oy 61 ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysIleCys 80
Db 994 AGAATTGGAGACACCTGGAGCAAGAGGATAATCGAGGAACCTGTCTCCAGTGCATCTGC 1053
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Qy	1	ProilAalaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr	20
Db	1209	CCCATAGCTGAGAAAGTGTGTTTGATCATGCTGCTGGAGACTTCTATGTGGTCGAGAAACG	1368
Qy	21	TrpGluLysProTyrGlnGlyTrrpMetMetValAspCysThrCysLeuGlyGluGlySer	40
Db	1269	TGGGAGAAGCCCTACCAAGGCTGGATGGTATGTTGTACTTGCCTGGGAGAAGGCAGC	1328
Qy	41	GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr	60
Db	1329	GGACGGATCATCTTGCACCTCTCAGAAATAGATGCAACGATCAGGACACAAGGACATCCTAT	1388
Qy	61	ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys	80
Db	1389	AGAAATTGGAGACACCTTGGACCAAGAGATTAATCGAGAAACCTTGCTCCAGTGCATCTGC	1448
Qy	81	ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer	100
Db	1449	ACAGGCAACGGCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGCAGACCCACATCG	1508
Qy	101	SerGlySerGlyProPheThrAspValArg	110
Db	1509	AGCGGATCTGGCCCTTACCGATGTTGCT	1538

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RESULT 12
US-09-581-651B-41
; Sequence 41, Application US/09581651B
; GENERAL INFORMATION:
; APPLICANT: University of Dundee, University of Dundee
; TITLE OF INVENTION: Polypeptides, Polynucleotides and Uses Thereof
; FILE REFERENCE: 350013-72
; CURRENT APPLICATION NUMBER: US/09/581,651B
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/GB98/03766
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-581-651B-41

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Alignment Scores:			
Pred. No.:	1.12e-54	Length:	1926
Score:	627.00	Matches:	110
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	25	Gaps:	0

US-09-940-235-4 COPY 150 259 (1-110) x US-09-581-651B-41 (1-1926)

	QY	1	ProIlaalagLylusCysPheaspHisAlaAaGlyThrSerTyrValValGlyGluThr	20
	Db	541	CCCATAGCTGAGAAGTGTTTTGTATCATGCTCGGCACCTCCTATGTGTGTCGGAGAACG	600
	QY	21	TrrpGlulAspProtyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGluGlySer	40
	Db	601	TGGGAGAACCCCTACCAGAGCTGGATGGATGGTAGATTGACTTTGCTTGGGAGAAAGCAGC	650

Qy	41	GlyArgIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr	60
Db	661	GGAGCGCATCATTGCACTTCTAGAAATAGATGCAACGATCAGGACACAGGCATCCTAT	720
Qy	61	ArgIleGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuLeuGlnCysIleCys	80
Db	721	AGAATTGGAGACACCTGGAGCAGGAAGGATAATCGAGGAAACCTGTCTCCAGTGCATCTGC	780
Qy	81	ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer	100
Db	781	ACAGGCAACGGCGGAGAGAGTGGAGTGTGAGAGGCACACCTCTGTGCAGACCATCG	840

```

Qy      101 SerGlySerGlyProPheThrAspValArg 110
      |||||
Db      841 AGCGGATCTGGCCCCCTTCACCGATGTCGT 870

RESULT 13
US-09-581-651C-41
; Sequence 41, Application US/09581651C
; GENERAL INFORMATION:
; APPLICANT: Schor, Seth Lawrence
; APPLICANT: Schor, Ana Maria
; TITLE OF INVENTION: Polypeptides, Polynucleotides and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: ERPO1.003APC
; CURRENT APPLICATION NUMBER: US/09/581,651C
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: PCT/GB98/03766
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: GB 9726539.1
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-581-651C-41

```

Alignment Scores:		
Pred. No.:	1,12e-54	Length:
Score:	627.00	Matches:
Percent Similarity:	100.00%	Conservative:
Best Local Similarity:	100.00%	Mismatches:
Query Match:	100.00%	Indels:
DB:	25	Gaps:

US-09-940-235-4 COPY 150 259 (1-110) x US-09-581-651C-41 (1-1926)

Qy	1	Pro	I	A	L	A	G	L	u	L	y	S	e	S	P	h	e	S	A	L	a	L	a	G	L	y	T	h	r	S	e	r	T	y	r	V	a	L	G	L	y	G	L	u	T	h	r	20							
Db	541	C	C	C	A	T	A	G	C	T	G	A	A	G	T	G	T	T	T	T	G	A	T	C	A	T	G	C	T	G	C	T	G	G	A	C	T	T	C	T	A	T	G	T	G	C	G	A	A	A	C	G	600		
Qy	21	T	r	p	G	L	u	L	y	P	r	o	f	r	y	G	L	i	n	G	L	y	T	r	p	M	e	t	V	a	L	A	s	p	C	y	S	e	L	e	u	G	L	y	G	L	u	S	e	r	40				
Db	601	T	G	G	A	G	A	G	C	C	T	T	A	C	A	A	G	G	C	T	G	G	A	T	G	T	G	T	A	G	T	T	G	A	T	T	G	A	T	T	G	C	T	C	T	G	C	G	A	A	G	C	A	G	660

QY 41 GlyArgIleIleThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 661 GGAGCGCATCAGTTCGACTTCTAGAAATAGATGCAACGATCAGGACACAGGACATCCTAT 720
QY 61 ArgIleGlyAspThrTrpSerIleWslvsAspAsnArgGlyVasnLeuLeuGlnCysIleCys 80

db 721 AGAATTGGAGACACCTGGAGCAAGGATAATCGAGGAAACCTGCTCCAGTGCACTGC 780

Qy	81	ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer	100
Db	781	ACAGGCAACGGCCGAGAGAGTGGAGTGATGAGAGCACCTCTGTGCAGACCATCG	840
Qy	101	SerGlySerGlyProPheThrAspValArg	110
Db	841	AGCGGATCTGGCCCTTCACCGATGTTCTG	870

RESULT 14
US-09-471-349-12
; Sequence 12, Application US/09471349
; GENERAL INFORMATION:
; APPLICANT: Sahni, Girish
; APPLICANT: Kumar, Rajesh
; APPLICANT: Roy, Chaiti
; APPLICANT: Rajagopal, Kammarra
; APPLICANT: Niharani, Deepak
; APPLICANT: Sundaram, Vasudha
; APPLICANT: Yadav, Mahavir

;; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE PROTEINS POSSESSING ALTERED
;; TITLE OF INVENTION: PLASMINOGEN ACTIVATION CHARACTERISTICS AND A PROCESS FOR THE
;; TITLE OF INVENTION: PREPARATION OF SAID PROTEINS
;; FILE REFERENCE: 07064/009001

;; CURRENT APPLICATION NUMBER: US/09/471,349

;; CURRENT FILING DATE: 1999-12-23

;; PRIOR APPLICATION NUMBER: IN 3825/DEL/98

;; PRIOR FILING DATE: 1998-12-24

;; NUMBER OF SEQ ID NOS: 24

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 12

;; LENGTH: 2096

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Synthetically generated primer

US-09-471-349-12

Alignment Scores:
Pred. No.: 1.23e-54 Length: 2096
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-471-349-12 (1-2096)

Qy 1 ProileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 1764 CCATAGCTGAGAAGTGTCTTGGATCATGCTGCTGGACTTCTCTATGTGTGGGAGAAACG 1823
Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 1824 TGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTTACTTCCCTGGGAGAAAGGCAGC 1883
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 1884 GGAGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACACAGGACATCCTAT 1943
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysileCys 80
Db 1944 AGAATTGGAGACACCTGGAGCAGAGAGATAATCGAGGAAACCTGCTCCAGTGCATCTGC 2003
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 2004 ACAGCAACGCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 2063
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 2064 AGCGATCTGGCCCTTCACCGATGTTCTGT 2093

RESULT 15

US-09-940-235-12

;; Sequence 12, Application US/09940235

;; GENERAL INFORMATION:

;; APPLICANT: Kumar, Rajesh

;; APPLICANT: Sahni, Girish

;; APPLICANT: Roy, Chait

;; APPLICANT: Rajagopal, Kammar

;; APPLICANT: Nihalani, Deepak

;; APPLICANT: Sundaram, Vasudha

;; APPLICANT: Yadav, Mahavir

;; TITLE OF INVENTION: NOVEL CLOT-SPECIFIC STREPTOKINASE

;; TITLE OF INVENTION: PROTEINS POSSESSING ALTERED PLASMINOGEN ACTIVATION

;; TITLE OF INVENTION: CHARACTERISTICS AND A PROCESS FOR THE PREPARATION OF SAID

;; TITLE OF INVENTION: PROTEIN

;; FILE REFERENCE: 07064-009002

;; CURRENT APPLICATION NUMBER: US/09/940,235

;; CURRENT FILING DATE: 2002-04-09

;; PRIOR APPLICATION NUMBER: 09/471,349

;; PRIOR FILING DATE: 1999-12-23

;; PRIOR APPLICATION NUMBER: IN 3825/DEL/98

;; PRIOR FILING DATE: 1998-12-24
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 12
;; LENGTH: 2096

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Hybrid cassette

US-09-940-235-12

Alignment Scores:
Pred. No.: 1.23e-54 Length: 2096
Score: 627.00 Matches: 110
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 40 Gaps: 0

US-09-940-235-4_COPY_150_259 (1-110) x US-09-940-235-12 (1-2096)

Qy 1 ProfileAlaGluLysCysPheAspHisAlaAlaGlyThrSerTyrValValGlyGluThr 20
Db 1764 CCATAGCTGAGAAGTGTCTTGGATCATGCTGCTGGACTTCTCTATGTGTGGGAGAAACG 1823
Qy 21 TrpGluLysProTyrGlnGlyTrpMetMetValAspCysThrCysLeuGlyGlySer 40
Db 1824 TGGAGAAGCCCTACCAAGGCTGGATGATGTAGATTGTTACTTCCCTGGGAGAAAGGCAGC 1883
Qy 41 GlyArgileThrCysThrSerArgAsnArgCysAsnAspGlnAspThrArgThrSerTyr 60
Db 1884 GGAGCATCACTTGCACCTTCTAGAAATAGATGCAACGATCAGGACACACAGGACATCCTAT 1943
Qy 61 ArgileGlyAspThrTrpSerLysLysAspAsnArgGlyAsnLeuGlnCysileCys 80
Db 1944 AGAATTGGAGACACCTGGAGCAGAGAGTGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 2003
Qy 81 ThrGlyAsnGlyArgGlyGluTrpLysCysGluArgHisThrSerValGlnThrThrSer 100
Db 2004 ACAGCAACGCCGAGGAGAGTGAAGTGTGAGAGGCACACCTCTGTGCAGACCACATCG 2063
Qy 101 SerGlySerGlyProPheThrAspValArg 110
Db 2064 AGCGATCTGGCCCTTCACCGATGTTCTGT 2093

Search completed: November 6, 2004, 07:38:48

Job time : 1804.68 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:49:35 ; Search time 4.14384 Seconds
(without alignments)
419.494 Million cell updates/sec

Title: US-09-940-235-4_COPY_150_259

Perfect score: 627

Sequence: 1 PIAKCFDHAAGTSYVVGCT.....ERHTSVQTTSSGSGPFTDVR 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 66696 seqs, 15802848 residues

Total number of hits satisfying chosen parameters: 66696

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents AA New:

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pcp.*
- 2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pcp.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pcp.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pcp.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pcp.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pcp.*
- 7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pcp.*
- 8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	627	100.0	657	1	PCT-US04-31524-365
2	627	100.0	2176	1	PCT-US04-31524-367
3	627	100.0	2296	1	PCT-US04-31524-371
4	627	100.0	2330	1	PCT-US04-31524-375
5	627	100.0	2355	1	PCT-US04-31524-191
6	627	100.0	2386	6	US-10-868-577A-59
7	627	100.0	2421	1	PCT-US04-31524-369
8	627	100.0	2476	1	PCT-US04-31524-373
9	213	34.0	211	6	US-10-868-577A-58
10	71.5	11.4	2157	6	US-10-960-275-2
11	70	11.2	1036	6	US-10-955-952-142
12	70	11.2	1036	6	US-10-157-779-142
13	70	11.2	1036	6	US-10-964-241-142
14	69.5	11.1	950	6	US-10-961-020-4
15	69	11.0	457	6	US-10-960-275-5
16	67	10.7	454	6	US-10-732-923-13429
17	67	10.7	802	6	US-10-732-923-13428
18	65	10.4	494	6	US-10-866-527-98
19	64	10.2	796	6	US-10-882-029-24
20	64	10.2	799	6	US-10-482-029-26
21	63.5	10.1	2871	6	US-10-967-702-390
22	62	9.9	201	6	US-10-732-923-14745
23	62	9.9	240	6	US-10-732-923-14746
24	61.5	9.8	54	4	US-08-828-323A-24
25	61.5	9.8	1067	6	US-10-650-650-18

ALIGNMENTS

RESULT 1

PCT-US04-31524-365

; Sequence 365, Application PC/TUS0431524

; GENERAL INFORMATION:

; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.

; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS

; FILE REFERENCE: DEN-054PC

; CURRENT APPLICATION NUMBER: PCT/US04/31524

; CURRENT FILING DATE: 2004-10-01

; PRIOR APPLICATION NUMBER: 60/506221

; PRIOR FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 60/509594

; PRIOR FILING DATE: 2003-10-08

; NUMBER OF SEQ ID NOS: 381

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 365

; LENGTH: 657

; TYPE: PRT

; ORGANISM: Homo sapiens

PCT-US04-31524-365

Query Match 100.0%; Score 627; DB 1; Length 657;

Best Local Similarity 100.0%; Pred. No. 7.2e-56;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PIAKCFDHAAGTSYVVGCTWEKPYQGMWVDCTCLGSGSGRITCTSRNRCNDQDTRTSY 60

Db 181 PIAKCFDHAAGTSYVVGCTWEKPYQGMWVDCTCLGSGSGRITCTSRNRCNDQDTRTSY 240

Qy 61 RIGTWSKKNRNLLQICITGNGRGEWKCERHTSVQTTSSGSGPFTDVR 110

Db 241 RIGTWSKKNRNLLQICITGNGRGEWKCERHTSVQTTSSGSGPFTDVR 290

RESULT 2

PCT-US04-31524-367

; Sequence 367, Application PC/TUS0431524

; GENERAL INFORMATION:

; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.

; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS

; FILE REFERENCE: DEN-054PC

; CURRENT APPLICATION NUMBER: PCT/US04/31524

; CURRENT FILING DATE: 2004-10-01

; PRIOR APPLICATION NUMBER: 60/506221

; PRIOR FILING DATE: 2003-09-25

; PRIOR APPLICATION NUMBER: 60/509594

; PRIOR FILING DATE: 2003-10-08

; NUMBER OF SEQ ID NOS: 381

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 2176
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-367

Query Match      100.0%; Score 627; DB 1; Length 2176;
Best Local Similarity 100.0%; Pred. No. 2.6e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
Db 181 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 240

Qy 61 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 110
Db 241 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 290

RESULT 3
PCT-US04-31524-371
; Sequence 371, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371
; LENGTH: 2296
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-371

Query Match      100.0%; Score 627; DB 1; Length 2296;
Best Local Similarity 100.0%; Pred. No. 2.8e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
Db 181 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 240

Qy 61 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 110
Db 241 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 290

RESULT 4
PCT-US04-31524-375
; Sequence 375, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 2330
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-375

Query Match      100.0%; Score 627; DB 1; Length 2330;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
Db 181 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 240

Qy 61 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 110
Db 241 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 290

RESULT 5
PCT-US04-31524-191
; Sequence 191, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 2355
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-191

Query Match      100.0%; Score 627; DB 1; Length 2355;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
Db 181 PIAKCFDHAAGTSYVVGWETWPKYQGMWVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 240

Qy 61 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 110
Db 241 RIGDTSKDKNRGNLLQICITGNGRGEWKCEKERTHSVQTTSSGSGPPTDVR 290

RESULT 6
US-10-868-577A-59
; Sequence 59, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 59
; LENGTH: 2386
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)..(272)
; OTHER INFORMATION: heparin binding domain
US-10-868-577A-59
```

Query Match 100.0%; Score 627; DB 6; Length 2386;
Best Local Similarity 100.0%; Pred. No. 2.9e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
DB 181 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 240

QY 61 RIGTWSKDNKRNLLQICITGNGRGEWKCEHRTSVQTTSSGSGPFTDVR 110
DB 241 RIGTWSKDNKRNLLQICITGNGRGEWKCEHRTSVQTTSSGSGPFTDVR 290

RESULT 7
PCT-US04-31524-369
; Sequence 369, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 2421
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-369

Query Match 100.0%; Score 627; DB 1; Length 2421;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
DB 181 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 240

QY 61 RIGTWSKDNKRNLLQICITGNGRGEWKCEHRTSVQTTSSGSGPFTDVR 110
DB 241 RIGTWSKDNKRNLLQICITGNGRGEWKCEHRTSVQTTSSGSGPFTDVR 290

RESULT 8
PCT-US04-31524-373
; Sequence 373, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 2476
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-373

Query Match 100.0%; Score 627; DB 1; Length 2476;
Best Local Similarity 100.0%; Pred. No. 3e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
DB 180 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 239

QY 61 RIGTWSKDNKRNLLQICITGNGRGEWKCEHRTSVQTTSSGSGPFTDVR 110
DB 240 RIGTWSKDNKRNLLQICITGNGRGEWKCEHRTSVQTTSSGSGPFTDVR 289

RESULT 9
US-10-868-577A-58
; Sequence 58, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-58

Query Match 34.0%; Score 213; DB 6; Length 211;
Best Local Similarity 37.6%; Pred. No. 9.5e-15;
Matches 35; Conservative 17; Mismatches 39; Indels 2; Gaps 1;

QY 1 PIAKCFDHAAGTSYVVGTEWKEPYQGMMVDDCTCLGEGSGRITCTSRNRCDQDTRTSY 60
DB 26 PTDDSCFDPYTVSHYAVGDEWERMESGFKLLCQLGFGSGHFRCDSSRWCHDNG--VNY 83

QY 61 RIGTWSKDNKRNLLQICITGNGRGEWKCEH 93
DB 84 KIGEKWDKQNGQNGMMSCCTCLGNGKGEFKCDPH 116

RESULT 10
US-10-960-275-2
; Sequence 2, Application US/10960275
; GENERAL INFORMATION:
; APPLICANT: Hastings, et al.
; TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
; FILE REFERENCE: PF487
; CURRENT APPLICATION NUMBER: US/10/960,275
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/466,778
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/113,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 2157
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; LOCATION: (2058)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; LOCATION: (2109)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; LOCATION: (2126)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2122)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (2123)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-960-275-2

Query Match 11.4%; Score 71.5; DB 6; Length 2157;
Best Local Similarity 30.6%; Pred. No. 21;
Matches 30; Conservative 9; Mismatches 28; Indels 31; Gaps 7;
Qy 2 IAEEKCPHAGTSYVVGTEWKPQGMWVDCICLG--EGSGRITCTSRNRCNDQDRTS 59
Db 1678 VADLCQDGHGCGSEHANC-----QVGTWVCTCLPDYEGDG-WSCRARNPCTD----- 1725
Qy 60 YRIGDTWSKKDNKGNLIQ---CICGTG-NRGGEWKCEH 93
Db 1726 -----GHRGCGSEHANCSTGLNTR---RCECH 1750

RESULT 11
US-10-955-952-142
; Sequence 142, Application US/10955952
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C12
; CURRENT APPLICATION NUMBER: US/10/955,952
; CURRENT FILING DATE: 2004-09-29
; PRIOR APPLICATION NUMBER: US/10/121,058
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142

; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-955-952-142
Query Match 11.2%; Score 70; DB 6; Length 1036;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;
Qy 9 HAAGTSYVVGTEWKPQGMWVDCICLGSGRITCTSR-----CICLTGSGRITCTSR----- 48
Db 680 HAPGEYFVEGETWN-----IDSCVQCTC---HSGRLCETEVCPPLLCQNSRTOD 728
Qy 49 ---NRCDNDQDRTSYRIGDTWSKKDNKGNLIQCICTGNRGE-----WKGERHTS 95
Db 729 SCCPQCTDQPPRSL-----SRNNSVPNYCK-NDEGDIPLAESWKPVDVCTS 774
RESULT 12
US-10-157-779-142
; Sequence 142, Application US/10157779
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C426
; CURRENT APPLICATION NUMBER: US/10/157,779
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-157-779-142
Query Match 11.2%; Score 70; DB 6; Length 1036;

Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;
Qy 9 HAAGTSVW-GETWEKPYQGMVMD---CTCLGEGSGRITCTSR-----WKCRHSTS 95
Db 680 HAPGGYFVEGETWN-----IDSTQCTC---HSGRVLCTEVCVCPPLLCQNPSRTQD 728
Qy 49 ---NRNQDQTRTSYRIGDTWSKKDNRGNLLQICITGNRGE-----WKCRHSTS 95
Db 729 SCCPQCTDQPRPSL-----SRNNSVNPYCK-NDEGDIPLAESAESWKPDVCTS 774

RESULT 13
US-10-964-241-142
; Sequence 142, Application US/10964241
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C33
; CURRENT APPLICATION NUMBER: US/10/964,241
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: PRIORT APPLICATION NUMBER: US/10/123,236
; PRIOR FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 142
; LENGTH: 1036
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-964-241-142

Query Match 11.2%; Score 70; DB 6; Length 1036;
Best Local Similarity 26.5%; Pred. No. 13;
Matches 31; Conservative 8; Mismatches 26; Indels 52; Gaps 8;
Qy 9 HAAGTSVW-GETWEKPYQGMVMD---CTCLGEGSGRITCTSR-----WKCRHSTS 95
Db 680 HAPGGYFVEGETWN-----IDSTQCTC---HSGRVLCTEVCVCPPLLCQNPSRTQD 728

Qy 49 ---NRNQDQTRTSYRIGDTWSKKDNRGNLLQICITGNRGE-----WKCRHSTS 95
Db 729 SCCPQCTDQPRPSL-----SRNNSVNPYCK-NDEGDIPLAESAESWKPDVCTS 774
RESULT 14
US-10-961-020-4
; Sequence 4, Application US/10961020
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0241-USA
; CURRENT APPLICATION NUMBER: US/10/961,020
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/965,631
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/236,689
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-961-020-4
Query Match 11.1%; Score 69.5; DB 6; Length 950;
Best Local Similarity 19.7%; Pred. No. 14;
Matches 25; Conservative 18; Mismatches 45; Indels 39; Gaps 5;
Qy 12 GTSYVVGETWEK-----PYQGMVMDCT---CLGEGSGRITCTSRN-----49
Db 439 GASYTLQQCLAFGFGVSKPCPY-----MQYCTKLWCTGKAKGMVCTRHFPWADGTFSCG 494
Qy 50 -----RCNDQDTRTSYRIGDTWSKKDNRGNLLQICITGNRGEWKCRHSTS 101
Db 495 EGKCLKGACVNERHNLKRVDSWAKWDPYGP-----CSRCTGGGVQLARQCTNPTPA 549
Qy 102 GSGPFTD 108
Db 550 NGKYCE 556

RESULT 15
US-10-960-275-5
; Sequence 5, Application US/10960275
; GENERAL INFORMATION:
; APPLICANT: Hastings, et al.
; TITLE OF INVENTION: Novel Hyaluronan-Binding Proteins and Encoding Genes
; FILE REFERENCE: PF487
; CURRENT APPLICATION NUMBER: US/10/960,275
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/466,778
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: 60/113,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 5
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (359)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (409)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:

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; NAME/KEY: MISC FEATURE
; LOCATION: (420)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (422)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (423)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-960-275-5

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Query Match      11.0%; Score 69; DB 6; Length 457;
Best Local Similarity 34.3%; Pred. No. 6.8;
Matches 24; Conservative 6; Mismatches 14; Indels 26; Gaps 6;

Qy 30 MVDCTCLG--EGSGRITCTSRNRCNDQDTRTSYRIGDTWSKDNRGNLLQ---CICIG-N 83
Db 1 MVTCTCLPDYEGDG-WSCRARNPCTD-----GHRGGCSEHANCILSTGLN 43

Qy 84 GRGEWKCEH 93
Db 44 TR---RCECH 50

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Search completed: November 4, 2004, 00:11:50
Job time : 5.14384 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2004, 23:49:35 ; Search time 3.99315 Seconds
(without alignments)
419.494 Million cell updates/sec

Title: US-09-940-235-4_COPY_1_106

Perfect score: 600

Sequence: 1 QAQMVPQSPVAVSQSKPG.....SMIWDCTCIGAGRISCTI 106

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 66696 seqs, 15802848 residues

Total number of hits satisfying chosen parameters: 66696

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA New:
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep.*
8: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	596	99.3	657	1	PCT-US04-31524-365
2	596	99.3	2176	1	PCT-US04-31524-367
3	596	99.3	2296	1	PCT-US04-31524-371
4	596	99.3	2330	1	PCT-US04-31524-375
5	596	99.3	2355	1	PCT-US04-31524-191
6	596	99.3	2386	6	US-10-868-577A-59
7	596	99.3	2421	1	PCT-US04-31524-369
8	596	99.3	2476	1	PCT-US04-31524-373
9	162.5	27.1	211	6	US-10-868-577A-58
10	93	15.5	43	6	US-10-220-366A-21430
11	93	15.5	43	6	US-10-399-103A-811
12	75.5	12.6	1238	6	US-10-765-727-21
13	75.5	12.6	1238	6	US-10-846-989-55
14	75	12.5	950	6	US-10-961-020-4
15	72.5	12.1	1067	6	US-10-650-650-18
16	72.5	12.1	1218	6	US-10-765-727-20
17	72.5	12.1	1218	6	US-10-846-989-54
18	72.5	12.1	1218	6	US-10-650-650-1
19	71.5	11.9	2556	6	US-10-765-727-22
20	71.5	11.9	2556	6	US-10-846-989-56
21	70.5	11.8	376	6	US-10-732-923-12305
22	69.5	11.6	2471	6	US-10-765-727-23
23	69.5	11.6	2471	6	US-10-846-989-57
24	68.5	11.4	394	6	US-10-732-923-12479
25	68	11.3	167	6	US-10-954-094-131

26	68	11.3	258	6	US-10-954-094-117	Sequence 117, App
27	68	11.3	343	6	US-10-954-094-99	Sequence 99, Appl
28	68	11.3	434	6	US-10-954-094-85	Sequence 85, Appl
29	67.5	11.2	314	6	US-10-639-194-6	Sequence 6, Appli
30	67.5	11.2	394	6	US-10-732-923-12781	Sequence 12781, A
31	67.5	11.2	685	6	US-10-765-727-19	Sequence 19, Appl
32	67.5	11.2	685	6	US-10-846-989-53	Sequence 53, Appl
33	67.5	11.2	685	6	US-10-955-952-88	Sequence 88, Appl
34	67.5	11.2	685	6	US-10-157-779-88	Sequence 88, Appl
35	67.5	11.2	685	6	US-10-964-241-88	Sequence 88, Appl
36	67	11.2	2871	6	US-10-967-702-390	Sequence 390, App
37	66.5	11.1	394	6	US-10-732-923-12466	Sequence 12466, A
38	65.5	10.9	376	6	US-10-732-923-12280	Sequence 12280, A
39	65.5	10.9	392	6	US-10-732-923-12559	Sequence 12559, A
40	65.5	10.9	394	6	US-10-732-923-12806	Sequence 12806, A
41	65.5	10.9	394	6	US-10-732-923-12854	Sequence 12854, A
42	65.5	10.9	394	6	US-10-732-923-12855	Sequence 12855, A
43	64.5	10.8	394	6	US-10-732-923-12807	Sequence 12807, A
44	64.5	10.8	995	6	US-10-732-923-13678	Sequence 13678, A
45	64.5	10.8	1004	6	US-10-732-923-13677	Sequence 13677, A

ALIGNMENTS

RESULT 1
PCT-US04-31524-365
; Sequence 365, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 657
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-365

Query Match	99.3%	Score 596;	DB 1;	Length 657;
Best Local Similarity	99.1%	Pred. No. 2.8e-54;		
Matches 105;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;
Oy	1	QAQMVPQSPVAVSQSKPGCYDNGKHQIQINQWERTYILGNVLVCTCYGSGRGNCESKP	60	
Db	32	QAQMVPQSPVAVSQSKPGCYDNGKHQIQINQWERTYILGNVLVCTCYGSGRGNCESKP	91	
Oy	61	EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRISCTI	106	
Db	92	EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRISCTI	137	

RESULT 2
PCT-US04-31524-367
; Sequence 367, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 2176
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-367

Query Match          99.3%; Score 596; DB 1; Length 2176;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 3
PCT-US04-31524-371
; Sequence 371, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 371
; LENGTH: 2296
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-371

Query Match          99.3%; Score 596; DB 1; Length 2296;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 4
PCT-US04-31524-375
; Sequence 375, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 375
; LENGTH: 2330
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-375

Query Match          99.3%; Score 596; DB 1; Length 2330;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 5
PCT-US04-31524-191
; Sequence 191, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 2355
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-191

Query Match          99.3%; Score 596; DB 1; Length 2355;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 6
US-10-868-577A-59
; Sequence 59, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 59
; LENGTH: 2386
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)..(272)
; OTHER INFORMATION: heparin binding domain
US-10-868-577A-59
```

```

PCT-US04-31524-375

Query Match          99.3%; Score 596; DB 1; Length 2330;
Best Local Similarity 99.1%; Pred. No. 1.1e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 5
PCT-US04-31524-191
; Sequence 191, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 2355
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-191

Query Match          99.3%; Score 596; DB 1; Length 2355;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPQSPVAVSQSKPGCYDNGKHQYINQOWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGISCTI 137

RESULT 6
US-10-868-577A-59
; Sequence 59, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 59
; LENGTH: 2386
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)..(272)
; OTHER INFORMATION: heparin binding domain
US-10-868-577A-59
```


Query Match 99.3%; Score 596; DB 6; Length 2386;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPSPVAVSQSKPGCYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPSPVAVSQSKPGCYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 137

RESULT 7
PCT-US04-31524-369
; Sequence 369, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 2421
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-369

Query Match 99.3%; Score 596; DB 1; Length 2421;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPSPVAVSQSKPGCYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 32 QAOQWQPSPVAVSQSKPGCYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCSKP 91

Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 106
Db 92 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 137

RESULT 8
PCT-US04-31524-373
; Sequence 373, Application PC/TUS0431524
; GENERAL INFORMATION:
; APPLICANT: Dana-Farber Cancer Institute, Inc., et al.
; TITLE OF INVENTION: METHODS TO DETECT LINEAGE-SPECIFIC CELLS
; FILE REFERENCE: DFN-054PC
; CURRENT APPLICATION NUMBER: PCT/US04/31524
; CURRENT FILING DATE: 2004-10-01
; PRIOR APPLICATION NUMBER: 60/506221
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 60/509594
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 2476
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US04-31524-373

Query Match 99.3%; Score 596; DB 1; Length 2476;
Best Local Similarity 99.1%; Pred. No. 1.2e-53;
Matches 105; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QAOQWQPSPVAVSQSKPGCYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCSKP 60
Db 31 QAOQWQPSPVAVSQSKPGCYDNGKHQYINQWERTYLGVLVCTCYGSGRGFNCSKP 90
Qy 61 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 106
Db 91 EABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGRGISCTI 136

RESULT 9
US-10-868-577A-58
; Sequence 58, Application US/10868577A
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al.
; TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
; FILE REFERENCE: 28967/39359A
; CURRENT APPLICATION NUMBER: US/10/868,577A
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/478,390
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: US 10/669,176
; PRIOR FILING DATE: 2003-09-23
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 58
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-868-577A-58

Query Match 27.1%; Score 162.5; DB 6; Length 211;
Best Local Similarity 39.0%; Pred. No. 5e-10; Mismatches 28; Indels 7; Gaps 4;
Matches 32; Conservative 15;

Qy 21 CYDNGKHQYINQWERTYLGVLVCTCYGSGRG-FNCESKPEABETCFDKYTGNTYRVG 78
Db 76 CHDNGVNYKIGEKWDQNGEQMMSCTCLGNGKGEFKCDPH---EATCYD--DGKTYHVG 130
Qy 79 DTYERPKDSMIWDCICIGAGRG 100
Db 131 EQWQKEYLGAICCTCTCGGQRG 152

RESULT 10
US-10-366A-21430
; Sequence 21430, Application US/10220366A
; GENERAL INFORMATION:
; APPLICANT: HYSEQ, INC
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-042
; CURRENT APPLICATION NUMBER: US/10/220,366A
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 09/577,409
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/515,126
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 27802
; SOFTWARE: Custom
; SEQ ID NO 21430
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(43)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-10-220-366A-21430

Query Match 15.5%; Score 93; DB 6; Length 43;
Best Local Similarity 48.8%; Pred. No. 0.0013;
Matches 20; Conservative 3; Mismatches 18; Indels 0; Gaps 0;
Qy 59 KPEABETCFDKYTGNTYRVGDTYERPKDSMIWDCICIGAGR 99

Db 3 KPEPEKTCFNIQTGTYPCLSYEHSDSDXYVYVNRXLCAER 43

RESULT 11

US-10-399-103A-811
; Sequence 811, Application US/10399103A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-115/785
; CURRENT APPLICATION NUMBER: US/10399,103A
; CURRENT FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: PCT/US01/27760
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 09/687,527
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 892
; SOFTWARE: Custom
; SEQ ID NO 811
; LENGTH: 4315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-103A-811

Query Match 15.5%; Score 93; DB 6; Length 4315;
Best Local Similarity 31.6%; Pred. No. 0.22;
Matches 30; Conservative 12; Mismatches 39; Indels 14; Gaps 5;

Qy 8 PQSPVAVSQS-----KPGCYDNGKHQYINQWERTYVGNLVCTCYGSGRGFNCESK 60
Db 3540 PTPSPVPSSAPLSPSPAPGCDNAIPLRQVNETWT---LENC TVARCVGDN RVLLDPKP 3596

Qy 61 EAETCFDKYTGTYRVGDTYVERPKDSMWDCITCI 95

Db 3597 VANVTVCNKKHL--PIKVS DP-SQPCD-FHYECBCI 3627

RESULT 12

US-10-765-727-21
; Sequence 21, Application US/10765727
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MODULATORS OF NOTCH SIGNALLING FOR USE IN IMMUNOTHERAPY
; FILE REFERENCE: 674525-2010
; CURRENT APPLICATION NUMBER: US/10765,727
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: PCT/GB02/03426
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: GB 0118153.6
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: GB 0207930.9
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: GB 0212282.8
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: GB 0212283.6
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 21
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-765-727-21

Query Match 12.6%; Score 75.5; DB 6; Length 1238;
Best Local Similarity 27.8%; Pred. No. 3.5;
Matches 25; Conservative 8; Mismatches 30; Indels 27; Gaps 6;

Qy 21 CYDNGKHQYINQWERTYVGNLVCTCYGSGRGFNCESKPEAETCFDKYT---GNTYR 76

Db 683 CHSRGRCYD-----LVNDFYCACDDGKWKTKCHSR---EFQC-DAYTCSNGGTCTYD 729
Qy 77 VGDYTERPKDSMWDCITCIGAGRISCTI 106
Db 730 SGDTFR-----CACPPGWKGS-TCAV 749

RESULT 13

US-10-846-989-55
; Sequence 55, Application US/10846989
; GENERAL INFORMATION:
; APPLICANT: BODMER, MARK WILLIAM
; APPLICANT: BRIEND, EMMANUEL CYRILLE PASCAL
; APPLICANT: CHAMPION, BRIAN ROBERT
; APPLICANT: LENNARD, ANDREW CHRISTOPHER
; APPLICANT: MCKENZIE, GRAHAME JAMES
; APPLICANT: MCKENZO, SILVIA
; APPLICANT: TUGAL, TAWARA
; APPLICANT: YOUNG, LESLEY LYNN
; TITLE OF INVENTION: MEDICAL TREATMENT
; FILE REFERENCE: 654525-2012
; CURRENT APPLICATION NUMBER: US/10/846,989
; CURRENT FILING DATE: 2004-05-14
; PRIOR APPLICATION NUMBER: PCT/GB02/05133
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: GB 0127271.5
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: GB 0220913.8
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 55
; LENGTH: 1238
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-846-989-55

Query Match 12.6%; Score 75.5; DB 6; Length 1238;
Best Local Similarity 27.8%; Pred. No. 3.5;
Matches 25; Conservative 8; Mismatches 30; Indels 27; Gaps 6;

Qy 21 CYDNGKHQYINQWERTYVGNLVCTCYGSGRGFNCESKPEAETCFDKYT---GNTYR 76
Db 683 CHSRGRCYD-----LVNDFYCACDDGKWKTKCHSR---EFQC-DAYTCSNGGTCTYD 729

Qy 77 VGDYTERPKDSMWDCITCIGAGRISCTI 106

Db 730 SGDTFR-----CACPPGWKGS-TCAV 749

RESULT 14

US-10-961-020-4
; Sequence 4, Application US/10961020
; GENERAL INFORMATION:
; APPLICANT: Friddle, Carl Johan
; APPLICANT: Hilbun, Erin
; TITLE OF INVENTION: Novel Human Proteases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0241-USA
; CURRENT APPLICATION NUMBER: US/10/961,020
; CURRENT FILING DATE: 2004-10-08
; PRIOR APPLICATION NUMBER: US/09/965,631
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/236,689
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 950
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-961-020-4

Search completed: November 4, 2004, 00:11:49
Job time : 4.99315 secs